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 FILE LAST UPDATED: 18 Dec 1997 (001017 ED)

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L1 32100 SEA FILE=REGISTRY ABB=ON E...H/SQSP  
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 L 32000 SEA FILE=REGISTRY ABB=ON L4 OR L4  
 L 15100 SEA FILE=REGISTRY FAN: 159234-43-7, ABB=ON L4 OR L4  
 L4 17000 SEA FILE=REGISTRY ABB=ON L1 NOT L4  
 L 1141 SEA FILE=H APLIN ABB=ON L4  
 L 13900 SEA FILE=H APLIN ABB=ON L7  
 L13 17884 SEA FILE=H APLIN ABB=ON FATTY ACID#  
 L11 1204 SEA FILE=H APLIN ABB=ON L11(4A)DESATUR?  
 L12 4 SEA FILE=H APLIN ABB=ON (L1 OR L11 AND L11  
 L13 8 SEA FILE=H APLIN ABB=ON L11 AND MUTAT?  
 L14 11 SEA FILE=H APLIN ABB=ON L11 AND DELTA(W (15 OR 12)  
 L15 21 SEA FILE=H APLIN ABB=ON (L1 OR L11 AND L10  
 L16 1 SEA FILE=H APLIN ABB=ON L11 AND MUTAT?  
 L17 8 SEA FILE=H APLIN ABB=ON L11 AND DELTA(W (15 OR 12)  
 L18 1 SEA FILE=H APLIN ABB=ON L11 OR L14 OR L17  
 L11 3 SEA FILE=H APLIN ABB=ON L11 AND MUTANT?  
 L12 9 SEA FILE=H APLIN ABB=ON L11 AND MUTANT?  
 L13 4 SEA FILE=H APLIN ABB=ON L21 AND DELTA(W (12 OR 15)  
 L14 1 SEA FILE=H APLIN ABB=ON L11 OR L22 OR L23

=> d 124 1-19 bib abs ind

- 1997:628484 Document No. 107:316934 Rapid and transient induction of a parsley microsomal **.DELTA.12 fatty acid desaturase** mRNA by fungal elicitor. Kirsch, Christoph; Hahlbrock, Klaus; Schüsslich, Imre E. (Max-Planck-Institut für Strukturforschung, Abteilung Biochemie, Cologne, D-50929, Germany). Plant Physiol., 115(1), 283-289 (English) 1997. CODEN: PLPHAY. ISSN: 0032-0839. Publisher: American Society of Plant Physiologists.
- AB Treatment of cultured parsley (*Petroselinum crispum*) cells with a structurally defined peptide elicitor (Pep25) of fungal origin has previously been shown to cause rapid and large changes in the levels of various **desatd. fatty acids**. Two distinct parsley cDNAs were isolated sharing high sequence similarity with microsomal **omega-6 fatty acid desaturases** (FADs). One of them was functionally identified as a **.DELTA.12 FAD** by expression in the yeast *Saccharomyces cerevisiae*. Two dienoic fatty acids, hexadecadienoic and linoleic, which were not detectable in control cells, together constituted up to 1% of the total fatty acids in the transformed yeast cells. **.DELTA.12 FAD** mRNA accumulated rapidly and transiently in elicitor-treated parsley cells, protoplasts, and leaves. These and previous results indicate that **fatty acid desatn.** is an important early component of the complex defense response of parsley to attempted fungal infection.
- CC 11-1 (Plant Biochemistry)  
Section cross-reference(s): 3, 7
- ST parsley **fatty acid desaturase** fungal elicitor; infection fungi parsley **fatty acid desaturase**; Pep25 elicitor **fatty acid desaturase** parsley
- IT Phytoalexin-eliciting hormones  
EL: PAC (Biological activity or effector, except adverse); BIOL (Ecological study)  
(Pep25; rapid and transient induction of a parsley microsomal **.DELTA.12 fatty acid desaturase** mRNA by fungal elicitor)
- IT cDNA sequences  
(1c1 parsley microsomal **.DELTA.12 fatty acid desaturase** responsive to fungal elicitor)
- IT Protein sequences  
(1c1 parsley microsomal **.DELTA.12 fatty acid desaturase** responsive to fungal elicitor)
- IT Parsley (*Petroselinum crispum*)  
(rapid and transient induction of a parsley microsomal **.DELTA.12 fatty acid desaturase** mRNA by fungal elicitor)
- IT 197594-14-2 197594-15-3  
EL: BPR (Biological process); PRP (Properties); BIOL (Biological study); PROOC (Process)  
(omega acid sequence; rapid and transient induction of a parsley microsomal **.DELTA.12 fatty acid desaturase** mRNA by fungal elicitor)
- IT 181442-99-4, GenBank U71741 197698-97-3  
EL: BPR (Biological process); PRP (Properties); BIOL (Biological study); PROOC (Process)  
(nucleotide sequence; rapid and transient induction of a parsley microsomal **.DELTA.12 fatty acid desaturase** mRNA by fungal elicitor)
- IT 84628-1-9, **Fatty acid .DELTA.12-desaturase**  
EL: BPR (Biological process); PRP (Properties); BIOL (Biological study)  
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- study); PROC (Process)  
 (rapid and transient induction of a parsley microsomal  
 .DELTA.12 fatty acid  
 desaturase mRNA by fungal elicitor)
- IT 67826-35-4, Fatty acid .omega.-3  
 desaturase  
 EL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
 (Biological study)  
 (rapid and transient induction of a parsley microsomal  
 .DELTA.12 fatty acid  
 desaturase mRNA by fungal elicitor)
- L24 ANSWER 2 OF 19 RECAPLUS COPYRIGHT 1997 ACS  
 1997:610711 Document No. 127:26444: The oleate desaturase product of  
 the FAD2-N gene of hazel and its uses. Dani, Maria; Catello, Sergio  
 (Spremaertes S.A., Belg.; Ferrera S.P.A.). Eur. Pat. Appl. EP 794250  
 A1 970910, 39 pp. DESIGNATED STATES: E: BE, ES, FR, GB, IT, NL.  
 (English). COSEN: EPXXIW. APPLICATION: EP 97-103023 970226.  
 PRIORITY: CH 97-850 260114.
- AB The FAD2-N gene of hazel (*Corylus avellana* L.) coding for the .  
 DELTA.12 desaturase enzyme of the microsomal  
 fraction is cloned and characterized for use as a probe for the  
 isolation of other plant desaturase genes. The gene can also be  
 used to alter the desaturase levels and consequently the  
 fatty-acid compn. of a plant. Probes derived from  
 the Arabidopsis .DELTA.12 desaturase gene were  
 used to screen a hazel cDNA bank from ripe *Corylus avellana* cv. San  
 Giovanni in .land-da.FAPII.
- IC 12M 01N 13-4:  
 12S 01N015-41; 012N003-02; 012N015-10; 012Q001-68
- ICA A01H005-00
- CC 7-2 (Enzymes)  
 Section cross-reference(s): 7, 11, 17
- ST Delta12 desaturase gene FAD2N Corylus; hazel delta12 desaturase gene  
 FAD2N
- IT Genes (plant)  
 EL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
 (Biological study)  
 (FAD2-N; oleate desaturase product of FAD2-N gene of hazel and  
 its uses)
- IT INA sequences  
 cDNA sequences  
 (cf. .DELTA.12 desaturase of hazel; oleate  
 desaturase product of FAD2-N gene of hazel and its uses)
- IT Fats and glyceric oils, Biological studies  
 EL: AGE (Agricultural use); BOC (Biological occurrence); FFD (Food  
 or feed use); BIOL (Biological study); OCCU (Occurrence); USES  
 (Uses)  
 (hazelnut, cloning of desaturase gene for altering  
 fatty acid profile of; oleate  
 desaturase product of FAD2-N gene of hazel and its uses)
- IT Fatty acids, biological studies  
 EL: AGE (Agricultural use); BOC (Biological occurrence); FFD (Food  
 or feed use); BIOL (Biological study); OCCU (Occurrence); USES  
 (Uses)  
 (cf hazel, cloning of desaturase gene for altering profile of;  
 oleate desaturase product of FAD2-N gene of hazel and its uses)
- IT Protein sequence:  
 of .DELTA.12 desaturase of hazel; oleate  
 desaturase product of FAD2-N gene of hazel and its uses)
- IT Hazel (*Corylus avellana*)  
 oleate desaturase product of FAD2-N gene of hazel and its uses)
- IT Endoplasmic reticulum  
 (.DELTA.12 desaturase of hazelnut; oleate

- desaturase product of FAD2-N gene of hazel and its uses)
- IT 196217-78-4  
EL: AGR (Agricultural use); BSU (Biological study, unclassified);  
PRP (Properties); BIOL (Biological study); USES (Uses)  
(amino acid sequence; oleate desaturase product of FAD2-N gene of  
hazel and its uses)
- IT 196217-80-8  
EL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
(Biological study)  
(amino acid sequence; oleate desaturase product of FAD2-N gene of  
hazel and its uses)
- IT 196217-77-5 196217-78-3 196217-81-3  
EL: AGR (Agricultural use); BSU (Biological study, unclassified);  
BSU (Biological use, unclassified); PRP (Properties); BIOL  
(Biological study); USES (Uses)  
(nucleotide sequence; oleate desaturase product of FAD2-N gene of  
hazel and its uses)
- IT 58929-86-1, Oleate desaturase  
EL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
(Biological study)  
(oleate desaturase product of FAD2-N gene of hazel and its uses)

L24 ANSWER 3 OF 19 NCAPLUS COPYRIGHT 1997 ACS

1997:512056 Document No. 127:13734 Plants having mutant

sequences that confer altered **fatty acid**

profiles. DeBonte, R. Lorin; Fan, Zheyong; Loh, R.-T. Willie

(Cargill, Incorporated, USA; DeBonte, R. Lorin; Fan, Zheyong; Loh,

R.-T. Willie). PCT Int. Appl. WO 9721440 A1 970619, 37 pp.

DESIGNATED STATES: W: AL, AU, AT, AR, AU, BB, BG, BR, BY, CA, CH,  
CN, CU, DE, DK, EE, ES, FI, GB, GR, HU, IL, IC, JP, KE, PG, KP, KR,  
KZ, LM, LF, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT,  
RU, SA, SD, SE, SG, SI, SK, TH, TM, TR, TT, UA, UG, US, VN, AM,  
AZ, BY, BG, BR, BS, BU, CA, CH, CL, CN, CO, CR, CU, CY, CZ, DE,  
DK, EE, EG, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, NL, HR, NE, NL,  
PT, SE, SN, TH, TG. (English). COHEN: PIXXD. APPLICATION: WO  
96-031095 961214. PRIORITY: US 95-17027 951214.

AB Seeds, plants and oils are provided having low FDA sats., high oleic  
acid, low linoleic acid,; high or low palmitic acid, low stearic  
acid, and low linoleic acid plus linolenic acid, and advantageous  
functional or nutritional properties. Plants are disclosed that  
contain a **mutation** in a **delta-12** or

**delta-15 fatty acid**

**desaturase** gene. Preferred plants are rapeseed and

sunflower plants. Plants carrying such **mutant** genes have

altered **fatty acid** compn. in seeds. In one

embodiment, a plant contains a **mutation** in a region having

the conserved motif His-Xaa-Xaa-Xaa-His, found in **delta-**

**12 and delta-15 fatty**

**acid desaturases**. A preferred motif has the

sequence His-Glu-Cys-Gly-His. A preferred **mutation** in

this motif has the amino acid sequence His-Lys-Cys-Gly-His. Nucleic

acid fragments are disclosed that comprise a **mutant**

**delta-12 or delta-15**

**fatty acid desaturase** gene sequence.

IC ICM A01H011-16

ICS A01H005-10; A01H011-40; C12N015-03; C07C037-02; C07C037-03;

C07C033-126

CC 1-9 Food and Feed Chemistry)

Section cross-reference(s): 11

ST **fatty acid** profile alteration plant

**mutation**; Brassica **fatty acid** profile

alteration **mutation**; Helianthus **fatty**

**acid** profile alteration **mutation**

IT Pollination

(cross; plants having **mutant** sequences that confer altered **fatty acid** profiles)

IT Genes

PL: PAC (Biological activity or effector, except adverse); BIOL (Biological study)

(microsomal; plants having **mutant** sequences that confer altered **fatty acid** profiles;

IT Brassica campestris

Brassica napus

Cruciferae (Brassicaceae)

Helianthus

Mitogenesis

**Mutation**

(plants having **mutant** sequences that confer altered **fatty acid** profiles)

IT **Fatty acids, biological studies**

PL: BOC (Biological occurrence); BPE (Biological process); BIOL (Biological study); OCCU (Occurrence); PROC (Process)

(plants having **mutant** sequences that confer altered **fatty acid** profiles)

IT Vegetable oils

PL: BOC (Biological occurrence); BEM (Removal or disposal); BIOL (Biological study); OCCU (Occurrence); PROC (Process)

(plants having **mutant** sequences that confer altered **fatty acid** profiles)

IT Candle oil

PL: BPE (Biological process); BIOL (Biological study); PROC (Process)

(plants having **mutant** sequences that confer altered **fatty acid** profiles)

IT 01-80-8, Ethylmercaptosulfonate 71427-04-8, .DELTA.

**15-Fatty acid desaturase**

11536-78-8, .DELTA.12-Fatty acid desaturase 192881-61-1 192881-62-6

192881-63-7 192881-64-8

PL: PAC (Biological activity or effector, except adverse); BIOL (Biological study)

(plants having **mutant** sequences that confer altered **fatty acid** profiles)

IT 192889-74-0 192889-75-1 192889-76-2 192889-77-3

192889-78-4 192889-79-5 192889-80-6 192889-81-9

PL: PAC (Biological activity or effector, except adverse); BPE (Biological process); BIOL (Biological study); PROC (Process)

(plants having **mutant** sequences that confer altered **fatty acid** profiles)

IT 37-10-3, Palmitic acid, biological studies 37-11-4, Stearic acid, biological studies

60-13-2, Linoleic acid, biological studies

115-10-1, Oleic acid, biological studies 463-40-1,

alpha-Linolenic acid 192823-14-4 192823-15-5 192823-16-6

192823-17-7 192823-18-8

PL: BOC (Biological occurrence); BIOL (Biological study); OCCU (Occurrence)

(plants having **mutant** sequences that confer altered **fatty acid** profiles)

L24 ANSWER 4 OF 1: NCAPLUS COPYRIGHT 1997 AIS

1997: 51385 Document No. 126:233-96 Microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of gamma-linolenic acid. Thomas, Terry L.; Reedy, Aratu S.; Nuccio, Michael; Kurbang, Andrew W.; Freyssinet, Georges L. (Rhône-Poulenc Agrochimie, Fr.). U.S. US 5614331 A 970325, 30 pp. Cont.-in-part of U.S. 5,552,396. (English). CODEN: USKKAM. APPLICATION: US 94-366773 941230. PRIORITY: US 91-334473 911010; US 92-817919 920108; US 93-959952 921013; US 94-307382 940914.

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AB Microbial genes for .DELTA.6-desaturases are cloned and characterized for use in the prepn. of transgenic organisms synthesizing high levels of .gamma.-linolenic acid from linoleic acid. Plants expressing a desaturase gene and with high tissue levels of .gamma.-linolenic acid are chilling resistant. These plants can also be used to produce oils with altered levels .gamma.-linolenic acid. The Synechocystis .DELTA.6-desaturase was cloned by expression in a .gamma.-linolenate-deficient Anabena. Expression of the gene in transgenic tobacco and carrot is demonstrated.

IC ICM 12N013-63  
ICM 12N013-62; C12N001-21; C12P007-64

NCL 439134006

CC 7-1. (Enzymes)

ST delta: desaturase gene Synechocystis borage; gamma linolenate manuf  
delta: desaturase

IT Plasmid vectors  
(1.1.1.DELTA.6NOS, borage .DELTA.6-desaturase gene on, expression in carrot cell culture and tobacco of; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)

IT Plasmid vectors  
(2.1.1.DELTA.6NOS, borage .DELTA.6-desaturase gene on, expression in carrot cell culture and tobacco of; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)

IT Carrot  
(cell cultures as expression host; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)

IT Corn  
Filamentous fungi  
Pearl  
Rape (plant)  
Soybean  
Sunflower  
Tobacco  
(expression host; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)

IT Arabidopsis  
(expression of .DELTA.6-desaturase genes from carboxylase promoter of; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)

IT Glycins  
EL: MSC (Miscellaneous)  
(expression of .DELTA.6-desaturase genes from promoter of gene for; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)

IT 35S promoter (genetic element)  
EL: BTU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(expression of .DELTA.6-desaturase genes from; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)

IT DNA sequences  
(for .DELTA.6-desaturase of Synechocystis; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)

IT cDNA sequences  
(for .DELTA.6-desaturase of borage; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)

- IT Genes (microbial)  
Genes (plant)  
EL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)  
(for .DELTA.6-desaturase, cloning and -expression of; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT Globulins, miscellaneous  
EL: MSC (Miscellaneous)  
(helianthins, expression of .DELTA.6-desaturase genes from promoter of gene for; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT Globulins, miscellaneous  
EL: MSC (Miscellaneous)  
(helianthins, expression of .DELTA.6-desaturase genes from promoter of gene for; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT Promoter (genetic element)  
EL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(homologous and heterologous, expression of .DELTA.6-desaturase genes from; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT Albumins, miscellaneous  
EL: MSC (Miscellaneous)  
(usapins, expression of .DELTA.6-desaturase genes from promoter of gene for; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT Protein sequences  
(of .DELTA.6-desaturases of *Synechocystis* and borage; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT Cold stress (plant)  
(transgenic plants resistant to; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT *Borago officinalis*  
*Synechocystis*  
(.DELTA.6-desaturase gene of; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT **148734-39-8 180583-92-0, Desaturase, linoleate**  
(*Borago officinalis*)  
EL: AGE (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)  
(amino acid sequence; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT 9031-31-4, Carboxylase  
EL: MSC (Miscellaneous)  
(expression of .DELTA.6-desaturase genes from *Anabaena* promoter of gene for; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT 7142-04-8, **.DELTA.15-Desaturase**  
8462-81-8  
EL: AGE (Agricultural use); BPN (Biosynthetic preparation); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)  
(gene for, in engineering **fatty acid** profiles; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)

- IT 91275-16-9P, Octadecatetraenoic acid  
 RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)  
 (manuf. with transgenic microorganisms, .DELTA.6-desaturase genes in; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT 9032-66-0P, .DELTA.6-Desaturase  
 RL: AGR (Agricultural use); BPN (Biosynthetic preparation); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)  
 (microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT 433-48-1, .alpha.-Linolenic acid  
 RL: BPN (Biological study, unclassified); BIOL (Biological study)  
 (microorganisms producing, manuf. of .gamma.-linolenate with; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT 1-1993-30-1 19933-31-2 19933-31-3  
 RL: AGR (Agricultural use); BPN (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)  
 (nucleotide sequence; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT 506-26-1P, .gamma.-Linolenic acid  
 RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation); USES (Uses)  
 (prepn. from linoleic acid of; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT 00-31-1, 9,12-Octadecadienoic acid (C,Z -, reactions  
 RL: EOC (Reagent)  
 (.gamma.-linolenic acid prepn. from; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)

L24 ANSWER 5 OF 15 READINGS COPYRIGHT 1997 ACS

1997: 12361 Document No. 126: 90447 Temperature-regulated mRNA accumulation and stabilization for **fatty acid desaturase** genes in the cyanobacterium *Synechococcus* sp. strain PCC 7102. Sakamoto, Tetsuo; Bryant, Donald A. (Department of Biochemistry and Molecular Biology, The Pennsylvania State University, University Park, PA, 16802, USA). Mol. Microbiol., 1997, 12361-12363 (English) 1997. COCEN: HOMIEE. ISSN: 1360-012X. Publisher: Blackwell.

AB Cyanobacteria adaptate to low-temp. conditions by desaturating their membrane lipids. The *desB* (omega-3 desaturase) and *desC* (.DELTA.12 desaturase) genes of *Synechococcus* sp. strain PCC 7102 were cloned and characterized, and the expression of the *desA* (.DELTA.12 desaturase), *desB* and *desC* genes was studied as a function of temp. The steady-state mRNA abundance for the *desA* gene was threefold higher in cells grown at 22.degree.C than in cells grown at 38.degree.C. *Desb* transcripts were not detected at 38.degree.C, but were abundant in cells grown at 22.degree.C. Levels of *desC* mRNA were similar at both growth temps. The mRNA levels of each desaturase gene increased within 15 min of a temp. shift-down to 22.degree.C, and mRNA level recovered within 15 min after a shift-up to 38.degree.C. The cold-induced accumulation of transcripts from the *desA* and *desb* genes was suppressed by the addn. of chloramphenicol, but the transient elevation of the *desC* transcript levels at 22.degree.C was not affected by chloramphenicol. The half-lives of the *desA* and *desB* mRNAs were significantly longer in cells grown at 22.degree.C than in cells grown at 38.degree.C, but the *desC* mRNA had a similar half-life at both temps. These studies reveal three patterns of temp. regulation

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for the desaturase genes, whose expression is tightly controlled by a combination of mRNA synthesis and stabilization. These studies demonstrate that elevation of desaturase mRNA levels is not the rate-limiting event during the low-temp. acclimation of cyanobacteria.

- CC 18-1 (Microbial, Algal, and Fungal Biochemistry)  
Section cross-reference(s): \*
- ST *Synechococcus* **fatty acid desaturase**  
gene sequence
- IT Genes (microbial)  
EC: PEP (Properties)  
DesA; temp.-regulated mRNA accumulation and stabilization for **fatty acid desaturase** genes in  
*cyanobacterium Synechococcus* sp. strain PCC 7002
- IT Genes (microbial)  
EC: PEP (Properties)  
DesA; temp.-regulated mRNA accumulation and stabilization for **fatty acid desaturase** genes in  
*cyanobacterium Synechococcus* sp. strain PCC 7002
- IT Genes (microbial)  
EC: PEP (Properties)  
DesA; temp.-regulated mRNA accumulation and stabilization for **fatty acid desaturase** genes in  
*cyanobacterium Synechococcus* sp. strain PCC 7002
- IT CNA sequences  
Protein sequences  
Synthetic genes  
Temperature effects (biological)  
temp.-regulated mRNA accumulation and stabilization for **fatty acid desaturase** genes in  
*cyanobacterium Synechococcus* sp. strain PCC 7002
- IT mRNA  
EC: PEP (Properties)  
temp.-regulated mRNA accumulation and stabilization for **fatty acid desaturase** genes in  
*cyanobacterium Synechococcus* sp. strain PCC 7002
- IT 156532-36-4  
EC: PEP (Properties)  
fatty acid sequence; temp.-regulated mRNA accumulation and stabilization for **fatty acid desaturase** genes in *cyanobacterium Synechococcus* sp. strain PCC 7002
- IT 156403-00-1, GenBank D13773 189176-00-2, GenBank U36389  
189178-00-1, GenBank U36391  
EC: PEP (Properties)  
nucleotide sequence; temp.-regulated mRNA accumulation and stabilization for **fatty acid desaturase** genes in *cyanobacterium Synechococcus* sp. strain PCC 7002
- IT 2014-34-0, **Fatty acid desaturase**  
EC: PEP (Properties)  
temp.-regulated mRNA accumulation and stabilization for **fatty acid desaturase** genes in  
*cyanobacterium Synechococcus* sp. strain PCC 7002

L24 ANSWER 6 OF 19 NCAPLUN COPYRIGHT 1997 ACS  
1996:7 3:3 Document No. 126:113911 The P-OLE1 gene of *Pichia angusta* encodes a  $\Delta^9$ -**fatty acid desaturase** and complements the  $\Delta^9$  mutation of *Saccharomyces cerevisiae*. Aramant, Sarinip; Tomita, Tetsushi; Fukui, Fumio; Fujimori, Ko; Harashima, Satoshi; Yamada, Yasuhiro; Oshima, Yasuji (Department of Biotechnology, Faculty of Engineering, Osaka University, 2-1 Yamadaoka, Suita-shi, Osaka, 565, Japan). Gene, 164(2), 295-306 (English) 1997. CODEN: GENED6. ISSN: 0378-1119.  
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Publisher: Elsevier.

- AB Three PCR-amplified DNA fragments hybridizing with the OLE1 gene encoding **.DELTA.9-fatty acid desaturase** of *Saccharomyces cerevisiae* were obtained using, resp., genomic DNAs of one strain each of *Kluyveromyces thermotolerans*, *Pichia angusta* and *Yarrowia lipolytica* as templates. A gene designated P-OLE1 was cloned from the above fragment of *P. angusta* and sequenced. An open reading frame of P-OLE1 encodes a 49.6-kDa protein consisting of 451 amino acid residues, which shows high identity (62) and similarity (19) to that deduced from the OLE1 nucleotide sequence. Expression of P-OLE1 driven by the *S. cerevisiae* GAP promoter or its own promoter complemented the ole1 **mutation** of *S. cerevisiae*. Transcription of P-OLE1 in the native host was suggested to be partially repressed by oleic acid in the medium, as was that of OLE1 in *S. cerevisiae* and a similar gene in *Y. lipolytica*, but that of a similar gene in *K. thermotolerans* was not.
- CC 3-3 (Biochemical Genetics)  
Section cross-reference(s): 7, 10
- ST P-OLE1 gene **fatty acid desaturase**  
sequence; *Pichia* **fatty acid desaturase**  
gene sequence
- IT Genes (microbial)  
EI: ANT (Analyte); BPA (Biological process); BPP (Properties); ANST (Analytical study); BIOL (Biological study); PPOC (Process)  
(P-OLE1; the P-OLE1 gene of *Pichia angusta* encodes a **.DELTA.9-fatty acid desaturase** and complements the ole1 **mutation** of *Saccharomyces cerevisiae*)
- IT Protein sequences  
(of *Pichia angusta* **.DELTA.9-fatty acid desaturase** 7)
- IT DNA sequences  
(of the P-OLE1 gene of *Pichia angusta* encoding a **.DELTA.9-fatty acid desaturase** and complementing the ole1 **mutation** of *Saccharomyces cerevisiae*)
- IT *Pichia angusta*  
*Saccharomyces cerevisiae*  
(the P-OLE1 gene of *Pichia angusta* encodes a **.DELTA.9-fatty acid desaturase** and complements the ole1 **mutation** of *Saccharomyces cerevisiae*)
- IT 112-33-1, Oleic acid, biological studies  
EI: BAC (Biological activity or effector, except adverse); BIOL (Biological study)  
(P-OLE1 gene of *Pichia angusta* encoding a **.DELTA.9-fatty acid desaturase** and complementing the ole1 **mutation** of *Saccharomyces cerevisiae* repressed by oleic acid)
- IT 186208-06-0  
EI: BAC (Biological activity or effector, except adverse); BPP (Properties); BIOL (Biological study)  
(Oleic acid sequence; the P-OLE1 gene of *Pichia angusta* encodes a **.DELTA.9-fatty acid desaturase** and complements the ole1 **mutation** of *Saccharomyces cerevisiae*)
- IT 186209-06-0  
EI: BPP (Properties)  
(nucleotide sequence; the P-OLE1 gene of *Pichia angusta* encodes a **.DELTA.9-fatty acid desaturase** and complements the ole1 **mutation** of *Saccharomyces cerevisiae*)
- IT P014-04-0, **.DELTA.9-Fatty acid desaturase**  
EI: BAC (Biological activity or effector, except adverse); BPP (Properties); BIOL (Biological study)

(the P-OLE1 gene of *Pichia angusta* encodes a .DELTA.9-  
fatty acid desaturase and complements  
the ole1 mutation of *Saccharomyces cerevisiae*)

L24 ANSWER 7 OF 13 HCAPLUS COPYRIGHT 1997 ACS

1996:23:644 Document No. 124:319.85 Isolation and characterization of  
an *Arabidopsis thaliana* cDNA encoding a .DELTA.7-sterol-C-5-  
desaturase by functional complementation of a defective yeast  
**mutant**. Gascotte, Daniel; Hasselstein, Tania; Bard, Martin;  
Lacroute, Francois; Benveniste, Pierre (Department de Biologie  
Cellulaire et Moleculaire, Institut de Botanique, Strasbourg, 67083,  
Fr.). Plant J., 9(3), 391-9 (English) 1996. CODEN: PLJED. ISSN:  
0950-7412.

AB A yeast null **mutant** (erg 3) defective in ERG 3, the gene  
encoding the C-5 sterol desaturase required for ergosterol synthesis  
was transformed with an *Arabidopsis thaliana* cDNA library inserted  
in a yeast vector. Transformants (4.times.10<sup>5</sup>) were screened for  
cycloheximide (CH) resistance and 400 possible clones were analyzed  
to det. their sterol profile. Low levels of ergosterol in addn. to  
.DELTA.7- and .DELTA.8-sterols normally present in erg3 were  
isolated in three yeast transformants. Characterization of one  
transformant indicated a cDNA of 1141 bp. Transformation of an erg  
3 strain with this plasmid led to CH resistance, nystatin  
sensitivity and an ergosterol profile. After sub-cloning in a  
pBlueScript vector and subsequent sequencing, an ORF of 843 bp  
encoding a possible 281 amino acid polypeptide was deduced. Three  
histidine-rich motifs (HX<sub>1</sub>H, HX<sub>2</sub>HH and HX<sub>3</sub>HH) were found in the A.  
*thaliana* ORF which are also present in the yeast ERG 3 gene. These  
histidine-rich motifs are also characteristic of many membrane-bound  
**fatty acid desaturases** from higher  
plants. These data strongly suggest that the A. *thaliana* cDNA  
encodes a .DELTA.7-sterol-C-5-desaturase.

CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 7, 11

ST *Arabidopsis* sterol desaturase cDNA sequence gene

IT Gene, plant

RL: PFP (Properties)

for C-5 sterol desaturase; isolation and characterization of  
*Arabidopsis thaliana* cDNA encoding .DELTA.7-sterol-C-5-desaturase  
by functional complementation of defective yeast **mutant**

IT *Arabidopsis thaliana*

Protein sequences

isolation and characterization of *Arabidopsis thaliana* cDNA  
encoding .DELTA.7-sterol-C-5-desaturase by functional  
complementation of defective yeast **mutant**.

IT Deoxyribonucleic acid sequences

complementary, isolation and characterization of *Arabidopsis*  
*thaliana* cDNA encoding .DELTA.7-sterol-C-5-desaturase by  
functional complementation of defective yeast **mutant**)

IT 175960-67-5

RL: PFP (Properties)

amino acid sequence contg. three histidine-rich motifs;  
isolation and characterization of *Arabidopsis thaliana* cDNA  
encoding .DELTA.7-sterol-C-5-desaturase by functional  
complementation of defective yeast **mutant**

IT 37215-37-1

RL: BUJ (Biological use, unclassified); BIOI (Biological study);  
USES (Uses)

isolation and characterization of *Arabidopsis thaliana* cDNA  
encoding .DELTA.7-sterol-C-5-desaturase by functional  
complementation of defective yeast **mutant**)

IT 170611-11-7, Genbank X90454

RL: PFP (Properties)

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(nucleotide sequence; isolation and characterization of  
*Arabidopsis thaliana* cDNA encoding .DELTA.7-sterol-C-5-desaturase  
 by functional complementation of defective yeast mutant  
 )

L24 ANSWER 3 OF 19 HCAPLUS COPYRIGHT 1997 ACS

1995:235099 Document No. 127:50097 Molecular cloning of cDNA for

**fatty acid desaturase** of *Anacyctis*

*nidulans* and its use in creating transgenic plant resistant to cold  
 temperature. Nishizawa, Osamu; Toguri, Toshihiro (Kirin Beer K. K.,  
 Japan). PCT Int. Appl. WO 94/22121 A1 950406, 41 pp. DESIGNATED  
 STATES: W: AM, AU, BB, BG, BR, BY, CA, CN, CZ, FI, GE, HU, JP, KG,  
 KR, KZ, LK, LU, LV, MD, MG, MN, NO, NZ, PL, RO, RU, SI, SK, TH, TT,  
 UA, US, UZ, VN; RW: AT, BE, BF, BI, CF, CG, CH, CI, CM, DE, DK, ES,  
 FR, GA, GB, GR, IE, IT, LB, MC, ML, MA, NE, NL, PT, SE, SN, TD, TG.  
 (Japanese). CODEN: PINKD2. APPLICATION: WO 94-JP22121 941223.  
 PRIORITY: JP 8-250855 931213.

AB Gene des 9 var fragment of *Anabaena variabilis* IAM N-3 is isolated  
 upstream from gene desA that encodes .DELTA.-12  
 -unsaturase and used as a probe for the isolation of open reading  
 frame (ORF) des 9 nia of *Anacyctis nidulans*. ORF des 9 nia codes  
 for a desaturase desaturating the .DELTA.-position of a fatty acid  
 bound to a lipid and exhibits 80 and 80% similarity to gene des 9  
 var of *Anabaena variabilis* and stearoyl-CoA unsaturase of mouse,  
 resp. The ORF introduced into transgenic tobacco plants increased  
 the content of unsatd. fatty acids and the resistance to cold temp.

IC 1CH: CLEN-13-13

IC3: CLEN-03-03; AG1H04-11; AG1H03-10

ICA CLEN-03-03

CC 7-8 (Enzymes)

Section cross-reference(s): 11

ST *Anacyctis* **fatty acid desaturase** cDNA

sequence; cold resistance des 9 nia *Anacyctis*; transgenic plant  
 unsatd fatty acid

IT Gene, plant

EL: AGE (Agricultural use); P&P (Properties); BIOL (Biological  
 study); USES (Uses).

des 9 nia; cloning of cDNA for .DELTA.9-fatty  
**acid desaturase** of *Anacyctis nidulans* and its  
 use in creating transgenic plant resistant to cold temp.)

IT Protein sequences

of .DELTA.9-fatty acid desaturase  
 of *Anacyctis nidulans*

IT Plant cell

Plant

Tobacco

transgenic; expression of cDNA for .DELTA.9-fatty  
**acid desaturase** of *Anacyctis nidulans* in

IT Temperature effects, biological

cold; expression of cDNA for .DELTA.9-fatty  
**acid desaturase** of *Anacyctis nidulans* in  
 transgenic plants to increase resistance to)

IT Deoxyribonucleic acid sequences

complementary, for .DELTA.9-fatty acid  
**desaturase** of *Anacyctis nidulans*)

IT Fatty acids, miscellaneous

EL: MSC (Miscellaneous)

unsatd., expression of cDNA for .DELTA.9-fatty  
**acid desaturase** of *Anacyctis nidulans* in  
 transgenic plants to increase content of)

IT 168613-13-6

EL: AGE (Agricultural use); P&P (Properties); BIOL (Biological  
 study); USES (Uses).

(amino acid sequence; cloning of cDNA for .DELTA.9-fatty

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- acid desaturase** of *Anacystis nidulans* and its use in creating transgenic plant resistant to cold temp.)
- IT 166922-04-3  
 EL: AGE (Agricultural use); PPE (Properties); BIOL (Biological study); USES (Uses)  
 (nucleotide sequence; cloning of cDNA for **.DELTA.9-fatty acid desaturase** of *Anacystis nidulans* and its use in creating transgenic plant resistant to cold temp.)
- L24 ANSWER 1 OF 13 NCAPLUS COPYRIGHT 1997 ACS  
 1995:27449 Document No. 12:24803 Identification of a gene that complements an *Arabidopsis* **mutant** deficient in chloroplast **.omega.6** desaturase activity. Falcone, Peane L.; Gibson, Susan; Lemieux, Bertrand; Somerville, Chris (Dep. Plant Biol., Carnegie Inst., Stanford, CA, 94305, USA). *Plant Physiol.*, 107(4), 1453-9 (English) 12-4. CODEN: PLIHAY. ISSN: 0032-0889.
- AB Membrane lipids of the **fad6** (formerly **fadC**) **mutant** of *Arabidopsis*, which is deficient in chloroplast **.omega.6** desaturase activity, have increased levels of monounsaturated **fatty acids** and are deficient in trienoic **fatty acids**. A putative **fad6** cDNA clone was isolated by probing a cDNA library with a degenerate oligonucleotide based on a conserved region within known **.omega.3** desaturase genes. Expression of the cDNA in transgenic plants of a **fad6 mutant** restored normal levels of all **fatty acids**. When used as a hybridization probe, the cDNA identified a restriction fragment-length polymorphism that co-segregated with the **fad6 mutation**. Thus, on the basis of a genetic complementation test and genetic map position, the **fad6** gene is encoded by the cDNA. The cDNA encoded a 418-amino acid polypeptide of 47,725 that displayed a high degree of sequence similarity to a **.DELTA.12** desaturase from the cyanobacterium *Synechocystis*. The **fad6** gene exhibited less sequence homol. to any known higher plant desaturase, including an endoplasmic reticulum-localized **.omega.6** desaturase corresponding to the *Arabidopsis* **fad2** gene.
- CC 7-8 Enzymes.  
 Section cross-reference(s): 1, 11
- ST **fatty acid .omega.6 desaturase** sequence  
*Arabidopsis*; cDNA **.omega.6** desaturase sequence *Arabidopsis* chloroplast; gene **fad6** sequence **.omega.6** desaturase *Arabidopsis*
- IT Gene, plant  
 EL: PPE (Properties)  
 (cloning; identification of gene that complements *Arabidopsis* **mutant** deficient in chloroplast **.omega.6** desaturase activity)
- IT *Arabidopsis thaliana*  
 Chloroplast  
 Leaf  
 Protein sequences  
 (identification of gene that complements *Arabidopsis* **mutant** deficient in chloroplast **.omega.6** desaturase activity)
- IT **Fatty acids**, biological studies  
 EL: BOC (Biological occurrence); NFM (Metabolic formation); BIOL (Biological study); FERM (Formation, nonpreparative); OCCU (Occurrence)  
 (identification of gene that complements *Arabidopsis* **mutant** deficient in chloroplast **.omega.6** desaturase activity)
- IT Deoxyribonucleic acid sequences  
 (complementary, identification of gene that complements *Arabidopsis* **mutant** deficient in chloroplast **.omega.6** desaturase activity)
- IT 163961-98-6

PL: BAC (Biological activity or effector, except adverse); PRP (Properties); BIOL (Biological study)  
 (identification of gene that complements Arabidopsis mutant deficient in chloroplast .omega.6 desaturase activity)

IT 66823-01-4, **Fatty acid .omega.6-Desaturase**

PL: BOC (Biological occurrence); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); OCCU (Occurrence)

(identification of gene that complements Arabidopsis mutant deficient in chloroplast .omega.6 desaturase activity)

IT 15573-04-6, GenBank U18 93

PL: PRP (Properties)

nucleotide sequence of; identification of gene that complements Arabidopsis mutant deficient in chloroplast .omega.6 desaturase activity)

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1995:16174 Document No. 12:134342 Cloning of .omega.3 desaturase from cyanobacteria and its use in altering the degree of membrane-lipid unsaturation. Sakamoto, Toshio; Lis, Dmitry A.; Higashi, Shoichi; Wada, Harume; Nishida, Ikio; Onmori, Masayuki; Kurate, Hario (Department Molecular Biomechanics, Graduate University Advanced Studies, Okazaki, 444, Japan). Plant Mol. Biol., 20(1), 249-57 (English) 1994. CODEN: PHEIEB. ISSN: 0167-4411.

AB Cyanobacteria respond to a decrease in temp. by **desaturating fatty acids** of membrane lipids to compensate for the decrease in membrane fluidity. Among various desatn. reactions in cyanobacteria, the desatn. of the .omega.3 position of **fatty acids** is the most sensitive to the change in temp. In the present study, the authors isolated a gene, designated *desB*, for the .omega.3 desaturase from the cyanobacterium, *Synechocystis* sp. PCC 6803. The *desB* gene encodes a protein a 359 amino-acid residue with mol. mass of 41.7 kDa. The *desB* gene is transcribed as a monocistronic operon that produced a single transcript of 1.4 kb. The level of the *desB* transcript in cells grown at 17.degree. was 10 times higher than that in cells grown at 24.degree.. To manipulate the **fatty-acid** unsatn. of membrane lipids, the *desB* gene in *Synechocystis* sp. PCC 6803 was **mutated** by insertion of a kanamycin-resistance gene cartridge. The resultant **mutant** was unable to **desaturate fatty acids** at the .omega.3 position. The *desA* gene, which encodes the .DELTA.12 desaturase of *Synechocystis* sp. PCC 6803, and the *desB* gene were introduced into *Synechococcus* sp. PCC 7942. While the parent cyanobacterium can only desaturate membrane lipids at the .DELTA.9 position of **fatty acids**, the resultant transformant was able to **desaturate fatty acids** of membrane lipids at the .DELTA.9, .DELTA.12 and .omega.3 positions. These results confirm the function of the *desB* gene and demonstrate that it is possible to genetically manipulate the **fatty-acid** unsatn. of membrane lipids in cyanobacteria.

CC 3-3 (Biochemical Genetics)

Section cross-reference 1): 7, 10

ST cloning sequence omega3 desaturase gene Synechocystis; Synechocystis desaturase alteration membrane lipid unsatn; gene desB sequence omega3 desaturase Synechocystis; transcription omega3 desaturase gene Synechocystis temp; desaturase delta12 omega3 Synechocystis transformation Synechococcus

IT Synechococcus

- Transformation, genetic  
 (alteration of membrane lipid unsatn. in *Synechococcus* sp. PCC 7941 by transformation with .omega.3- and .DELTA.
- IT 12 desaturase genes from *Synechocystis* sp. PCC 6813
- IT Lipids, biological studies  
 RL: MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)  
 (alteration of membrane lipid unsatn. in *Synechococcus* sp. PCC 7941 by transformation with .omega.3- and .DELTA.  
 12 desaturase genes from *Synechocystis* sp. PCC 6813)
- IT Fatty acids, biological studies  
 RL: MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)  
 (changes in fatty acid compn. of total lipids upon transformation of *Synechococcus* sp. PCC 7942 with .omega.3- and .DELTA.12 desaturase genes from *Synechocystis* sp. PCC 6813)
- IT *Synechocystis*  
 (cloning and sequence of .omega.3 desaturase from *Synechococcus* and its use in altering the degree of membrane-lipid unsatn.)
- IT Cell membrane  
 Deoxyribonucleic acid sequences  
 Protein sequences  
 (cloning and sequence of .omega.3 desaturase from *Synechocystis* and its use in altering the degree of membrane-lipid unsatn.)
- IT Cyanobacteria  
 (cloning and sequence of .omega.3 desaturase from cyanobacteria and its use in altering the degree of membrane-lipid unsatn.)
- IT Gene, microbial  
 RL: BPS (Biological process); PPS (Properties); BIOL (Biological study); PROC (Process)  
 (desB; cloning and sequence of .omega.3 desaturase gene desB from *Synechococcus* and its use in altering the degree of membrane-lipid unsatn.)
- IT Temperature effects, biological  
 (temp. regulation of .omega.3 desaturase gene desB transcript levels in *Synechocystis*)
- IT Ribonucleic acids, messenger  
 RL: MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)  
 (temp. regulation of .omega.3 desaturase gene desB transcript levels in *Synechocystis*)
- IT Gene, microbial  
 RL: BPS (Biological process); BIOL (Biological study); PROC (Process)  
 (desA, .DELTA.12 desaturase; alteration of membrane lipid unsatn. in *Synechococcus* sp. PCC 7941 by transformation with .omega.3- and .DELTA.12 desaturase genes from *Synechocystis* sp. PCC 6813)
- IT 1233-45-1, .DELTA.12 Desaturase  
 RL: BAC (Biological activity or effector, except adverse); BIOL (Biological study)  
 (alteration of membrane lipid unsatn. in *Synechococcus* sp. PCC 7941 by transformation with .omega.3- and .DELTA.12 desaturase genes from *Synechocystis* sp. PCC 6813)
- IT 17-1-3, Hexadecenoic acid, biological studies 37-11-4, C 18:0, biological studies 43-53-3, 9,12-Octadecadienoic acid (Z,Z)-, biological studies 113-50-1, 9-Octadecenoic acid (Z)-, biological studies 373-49-3, 9-Hexadecenoic acid, (Z)- 465-40-1 506-17-2, 11-Octadecenoic acid (Z)- 5070-15-1, 9,12-Hexadecadienoic acid, (Z,Z)- 28934-77-2, Octadecadienoic acid (Z,Z)- 32839-14-0  
 RL: BOC (Biological occurrence); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); OCCU (Occurrence)

(changes in **fatty acid** compn. of total lipids upon transformation of *Synechococcus* sp. PCC 7942 with  $\omega$ -3- and **.DELTA.12** desaturase genes from *Synechocystis* sp. PCC 6803)

IT 71427-24-3, **.DELTA.15** Desaturase  
**161027-24-3**

EL: EAC (Biological activity or effector, except adverse); PRP (Properties); BIOL (Biological study)  
(cloning and sequence of  $\omega$ -3 desaturase from cyanobacteria and its use in altering the degree of membrane-lipid unsat.)

IT 160234-15-7

EL: PRP (Biological process); PRP (Properties); BIOL (Biological study); PROC (Process)  
(cloning and sequence of  $\omega$ -3 desaturase from cyanobacteria and its use in altering the degree of membrane-lipid unsat.)

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1994:007897 Document No. 131:097899 Altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase. Gibson, Susan Irma; Kishore, Sanesh Murthy; Ruff, Thomas Gene; Somerville, Christopher Roland; Aronel, Vincent Jean-Marie Arnel Monsanto Co., USA; Michigan State University). ICT Int. Appl. WO 94/18137 A1 940818, 143 pp. DESIGNATED STATES: W: CA, GB, US, ES; BW: AT, BE, CH, DE, DK, ES, FR, GR, IE, IT, LU, NL, PT, SE. (English). CODEN: PIXXD2. APPLICATION: WO 94-US181 941214. PRIORITY: US 93-14431 910205; US 93-11051 911122.

AB The linolenic acid content of vegetable oils is altered by changing the levels of expression of linoleic acid desaturase, e.g. by expression of a heterologous gene or antisense gene for the enzyme. A cDNA for the enzyme derived from the *fad3* gene of *Brassica napus* was introduced into wild-type and *fad3* **mutants** of *Arabidopsis thaliana* by *Agrobacterium*-mediated transformation and transgenic plants prepd. Transformation of the wild type increased the linolenate content from 31.3 $\pm$ 4.3 to 51.3 $\pm$ 10.3 mol% of **fatty acids** and in the *fad3* **mutants** the increase was from 6.7 $\pm$ 1.7 to 43.1 $\pm$ 13.5 mol% of **fatty acids**.

IC 1CM 012N15-31

ICS 012N 15-53; 012N011-11; 012N101-11; A01H103-01; 011B101-00

CC 11-1 Plant Biochemistry

Section cross-reference : 3

ST linoleate desaturase plant linoleic acid level

IT *Arabidopsis thaliana*

(*fad3* gene of; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)

IT Gene, plant

EL: BIOL (Biological study)

(*fad3*, for linoleate desaturase of *Brassica napus*; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)

IT Gene, plant

EL: BIOL (Biological study)

(*fad3*, of *Arabidopsis thaliana*; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)

IT Gene, plant

EL: BIOL (Biological study)

(*fadD*, for linoleate desaturase of *Arabidopsis thaliana*; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)

IT Gene, plant

EL: BIOL (Biological study)

(*fadE*, for linoleate desaturase of *Arabidopsis thaliana*; altering

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- the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase
- IT Protein sequences  
(of linoleic acid desaturases of Arabidopsis and Brassica)
- IT Plasmid and Episome  
(pMON13801, pMON13803, expression vectors for plants; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT Plasmid and Episome  
(pMON13814, pMON13805, Brassica napus linoleate desaturase antisense gene on; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT Plasmid and Episome  
(pTIDES3, Brassica napus linoleate desaturase gene on; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT Plasmid and Episome  
(pTIDES3, linoleate desaturase gene of Arabidopsis thaliana on; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT Plant  
Paper (plant)  
Seed  
Soybean  
(transgenic; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT Plant stress  
(cold, improved resistance to; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT Deoxyribonucleic acid sequences  
(complementary, for linoleic acid desaturases of Arabidopsis and Brassica)
- IT Deoxyribonucleic acids  
FL: BVT (Biological use, unclassified); BIOL (Biological study);  
USES (Uses)  
(complementary, antisense, to fad3 gene for linoleate desaturase of Arabidopsis thaliana; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT Microorganism  
(phytopathogenic, improved resistance to; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT Fats and Glyceridic oils  
FL: PME (Bioindustrial manufacture); PRP (Properties); BIOL (Biological study); PREP (Preparation)  
(vegetable, altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT 112-41-1, 9-Octadecenoic acid (Z)-, biological studies 463-49-1, Linolenic acid 9052-06-0, Linoleic acid desaturase  
FL: AGE (Agricultural use); MEM (Metabolism formation); BIOL (Biological study); FORM (Formation, nonpreparative); USES (Uses)  
(altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT 148814-49-7 149955-97-5 158651-91-3  
FL: AGE (Agricultural use); PRP (Properties); BIOL (Biological study); USES (Uses)  
(amino acid sequence; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT F1427-(4-8), DELTA.15 Desaturase  
FL: AGE (Agricultural use); BOC (Biological occurrence); PRP  
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(Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses).

cloning of Arabidopsis thaliana gene for; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)

IT 13: 31-34-9 139203-33-0 119303-33-1

EL: AGR (Agricultural use); PRP (Properties); BIOL (Biological study); USES (Uses).

(nucleotide sequence; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)

L24 ANSWER 12 OF 19 HCAELUS COPYRIGHT 1997 ACS

1994:026646 Document No. 131:026646 Molecular cloning of cDNA for microsomal **delta-12 fatty acid**

**desaturases** and their use for molecular breeding of plants.

Lightner, Jonathan Edward; O'Leary, John Joseph (du Pont de Nemours, E. I., and Co., USA); Int. Appl. WO 941516 A1 940526, 147 pp.

DESIGNATED STATES: W: AU, BR, CA, CH, DE, ES, FR, GB, GR, IE, IT, LU, NL, PT, SE. (English). CODEN: EINDEX. APPLICATION: WO 94-23987 941013. PRIORITY: US 92-977339 921117.

AB The prepn. and use of nucleic acid fragments encoding **fatty acid desaturases** and related enzymes are

described. The invention permits alteration of plant lipid compn.

Chimeric genes incorporating such nucleic acid fragments with suitable regulatory sequences may be used to create transgenic plants with altered levels of unsatd. fatty acids. The cloning of

cDNA for **fatty acid .DELTA.12**

**-desaturases** (oleyl-CoA desaturases) from Arabidopsis

thaliana, Brassica napus, Glycine max, Zea mays, and Ricinus communis was demonstrated. The expression of antisense Gly max

**fatty acid .DELTA.12-**

**desaturase** cDNA in soybeans to reduce the expression of the enzyme in developing soybean seeds and use of the cDNA sequences for

restriction fragment length polymorphism (RFLP) mapping was also demonstrated.

IC 10M 010013-33

10M 010013-32; 010011-1 ; 010011-68; A01H005-00

CC 11-1 (Plant Biochemistry)

Section cross-reference(s): 1, 17

ST plant **fatty acid desaturase** cDNA

cloning; breeding lipid compn transgenic plant

IT Plant breeding and selection

cloning of **fatty acid desaturase**

cDNA in relation to)

IT Candi

Soybean

**fatty acid desaturase** expression

in; antisense cDNA for redn. of)

IT Protein sequences

of plant microsomal **fatty acid**

**desaturases**)

IT Plasmid and Episome

pPh1Fa2R, pZDFa2R, pZKFd2R, **fatty acid**

**desaturase** antisense cDNA of Brassica napus on, for

expression redn.)

IT Fats and Glyceridic oils

EL: PRP (Properties)

(transgenic plant cells having altered level of, cloning of

**fatty acid desaturase** in relation to)

IT Plant

(transgenic, unsatd. fatty acid level regulation in, cloning of

cDNA for **fatty acid desaturase** in

- relation to)
- IT Deoxyribonucleic acid sequences  
(complementary, for plant microsomal **fatty acid desaturases**)
- IT Deoxyribonucleic acids  
FL: BLOL (Biological study)  
(complementary, antisense, for **fatty acid desaturase**, for reducing **desaturase** gene expression in transgenic plants)
- IT Plasmid and Episome  
(pST11, **fatty acid desaturase** antisense cDNA of Glycine max on, for expression redn.)
- IT Genetic polymorphism  
(restriction fragment length, Genetic mapping, of gene for **fatty acid desaturase** of plants, cloning of **fatty acid desaturase** cDNA in relation to)
- IT Fatty acids, biological studies  
FL: PRP (Properties)  
(unsatd., transgenic plant cells having altered level of, cloning of **fatty acid desaturase** in relation to)
- IT 158283-24-0, .delta.-12 **Fatty acid desaturase** (*Arabidopsis thaliana* clone p9119) 158283-26-2, .delta.-12 **Fatty acid desaturase** (*Brassica napus* clone pCF2-165D) 158283-28-4, .delta.-12 **Fatty acid desaturase** (*Glycine max* clone pSFE-161K) 158283-30-8, .delta.-12 **Fatty acid desaturase** (*Zea mays* clone pFad2#1) 158283-32-0, .delta.-12 **Fatty acid desaturase** (*Ricinus communis* clone pSFE-10) 158283-34-2, .delta.-12 **Fatty acid desaturase** (*Ricinus communis* clone pRF197C-42)  
FL: BLOL (Biological study)  
(amino acid sequence of and cloning of cDNA for, mol. breeding in relation to)
- IT 77-51-31-3, Fatty acid .DELTA.12-hydroxylase  
FL: BLOL (Biological study)  
(gene for, method for cloning of)
- IT 84-01-31-3  
FL: BLOL (Biological study)  
(gene for, of plants, method for cloning of)
- IT 158283-31-3, DNA (*Arabidopsis thaliana* clone pAGE2-6 .delta.-12 **fatty acid desaturase** gene)  
FL: BLOL (Biological study); PRP (Properties)  
(nucleotide sequence and cloning of)
- IT 158283-10-7, DNA (*Arabidopsis thaliana* clone p92103 .delta.-12 **fatty acid desaturase** cDNA and flanks) 158283-25-1, DNA (*Brassica napus* clone pCF2-165D **fatty acid desaturase** cDNA and flanks) 158283-27-3, DNA (*Glycine max* clone pSFE-161K .delta.-12 **fatty acid desaturase** cDNA and flanks) 158283-29-5, DNA (*Zea mays* clone pFad2#1 .delta.-12 **fatty acid desaturase** cDNA and flanks) 158283-31-9, DNA (*Ricinus communis* clone pSFE-10 .delta.-12 **fatty acid desaturase** cDNA and flanks) 158283-33-1, DNA (*Ricinus communis* clone pRF197C-42 .delta.-12 **fatty acid desaturase** cDNA and flanks)  
FL: BLOL (Biological study); PRP (Properties)  
(nucleotide sequence and cloning of, mol. breeding in relation

- to)
- IT 141-12-1, Ricinoleic acid  
EL: PRP (Properties)  
(transgenic plant cells having altered level of, cloning of  
**fatty acid desaturase** in relation to)
- L24 ANSWER 13 OF 19 HCAPLUS COPYRIGHT 1997 ACS  
1994:63498L Document No. 121:224-92 Arabidopsis FAD2 gene encodes the  
enzyme that is essential for polyunsaturated lipid synthesis.  
Gidley, John; Lightner, Jonathan; Feldmann, Kenneth; Yadav,  
Narendra; Lark, Ellen; Brown, John (Inst. Biol. Chem., Washington  
State Univ., Pullman, WA, 99164-6340, USA. Plant Cell, 6 1),  
1994-09 (English) 1994. CODEN: PLOSEW. ISSN: 1040-4651.
- AB The polyunsatd. fatty acids linoleate and alpha.-linolenate are  
important membrane components and are the essential fatty acids of  
human nutrition. The major enzyme responsible for the synthesis of  
these compds. is the plant oleate desaturase of the endoplasmic  
reticulum, and its activity is controlled in Arabidopsis by the  
**fatty acid desatn.** (fad2 locus). A  
fad2 allele was identified in a population of Arabidopsis in which  
**mutations** had been created by T-DNA insertions. Genomic DNA  
fragments the T-DNA was cloned by plasmid rescue and used to isolate  
cDNA and genomic clones of FAD2. A cDNA contg. the entire FAD2  
~~coding sequence was expressed in fad2 mutant plants and~~  
shown to complement the **mutant** fatty acid phenotype. The  
deduced amino acid sequence from the cDNA showed homol. to other  
plant desaturases, and this confirmed that FAD2 is the structural  
gene for the desaturase. Gel blot analyses of FAD2 mRNA levels  
showed that the gene is expressed throughout the plant and suggest  
that transcript levels are in excess of the amt. needed to account  
for oleate desatn. Sequence anal. identified histidine-rich motifs  
that could contribute to an iron-binding site in the cytoplasmic  
domain of the protein. Such a position would facilitate interaction  
between the desaturase and cytochrome b5, which is the direct source  
of electrons for the desatn. reaction, but would limit interaction  
of the active site with the fatty acyl substrate.
- CC 7-1 (Enzymes)  
Section cross-reference(s) :
- ST gene FAD2, oleate desaturase sequence Arabidopsis; cDNA FAD2, oleate  
desaturase sequence Arabidopsis
- IT Arabidopsis thaliana  
(Arabidopsis FAD2 gene for oleate desaturase that is essential  
for polyunsatd. lipid synthesis)
- IT Gene, plant  
EL: BIOL (Biological study)  
(FAD2; Arabidopsis FAD2 gene for oleate desaturase that is  
essential for polyunsatd. lipid synthesis)
- IT Polyunsaturated acid sequences  
(of Arabidopsis FAD2 gene for oleate desaturase)
- IT Enzyme functional sites  
Protein sequences  
(of Arabidopsis FAD2 oleate desaturase)
- IT 514-13-1, Oleate desaturase  
EL: SAC (Biological activity or effector, except adverse); PRP  
(Properties); BIOL (Biological study)  
(Arabidopsis FAD2 gene for oleate desaturase that is essential  
for polyunsatd. lipid synthesis)
- IT 158283-24-0, Oleate desaturase Arabidopsis thaliana clone  
pFAD2 gene FAD2)  
EL: PRP (Properties)  
(amino acid sequence; Arabidopsis FAD2 gene for oleate desaturase  
that is essential for polyunsatd. lipid synthesis)
- IT 10241-16-7  
EL: PRP (Properties)

(nucleotide sequence; Arabidopsis FAD7 gene for oleate desaturase that is essential for polyunsatd. lipid synthesis)

L24 ANSWER 14 OF 19 HCAPLUS COPYRIGHT 1997 ACS

1994:471200 Document No. 121:74829 Identification of conserved domains in the **.DELTA.12** desaturases of cyanobacteria.

Sakamoto, Toshio; Wada, Hajime; Nishide, Ikuo; Ohmori, Masayuki; Murata, Hiroo (Dep. Mol. Biomechan., Univ. Advanced Studies, Okazaki, 444, Japan). Plant Mol. Biol., 14(4), 643-50 (English) 1994. CODEN: PMBIDE. ISSN: 0167-4411.

AB Cyanobacterial genes for enzymes that **desaturate fatty acids** at the **.DELTA.12**

position, designated desA, were isolated from Synechocystis PCC6714, Synechococcus PCC7002 and Anabaena variabilis by cross-hybridization with a DNA probe derived from the desA gene of Synechocystis PCC6708. The genes of Synechocystis PCC6714, Synechococcus PCC7002 and A. variabilis encode proteins of 149, 147 and 150 amino acid residues, resp. The transformation of Synechococcus PCC7042 with the desA genes from Synechocystis PCC6714, Synechococcus PCC7002 and A. variabilis was assod. with the ability to introduce a second double bond at the **.DELTA.12** position of fatty acids. The amino acid sequence of the products of the desA genes revealed the presence of four conserved domains. Since one of the conserved domains was also found in the amino acid sequences of **.omega.3** desaturases of Brassica napus and mung bean, this domain may play an essential role in the introduction of a double bond into fatty acids bound to membrane lipids.

CC E-3 (Biochemical Genetics)

Section cross-reference(s): 7, 11

ST desaturase gene desA sequence cyanobacteria; Anabaena Synechococcus Synechocystis desaturase gene sequence

IT Anabaena variabilis

(desaturase gene desA cf, updated nucleotide sequence of)

IT Synechococcus

Synechocystis

(gene desA cf, nucleotide and encoded peptide sequences of)

IT Deoxyribonucleic acid sequences

of desaturase gene desA, of Synechocystis and Synechococcus;

IT Protein sequences

of desaturase, of Synechocystis and Synechococcus)

IT Gen, microbial

RI: E101 (Biological study)

desA, for desaturase, of Synechocystis and Synechococcus, nucleotide and encoded peptide sequences of

IT 156532-35-3, Delta 12 desaturase

(Synechocystis PCC714) 156532-36-4, Delta

12 desaturase (Synechococcus PCC7002)

RI: PEP (Properties)

(amino acid sequence of)

IT 156462-28-6 156462-29-6 156471-40-5

RI: E101 (Biological study); PEP (Properties) nucleotide sequence of

L24 ANSWER 14 OF 19 HCAPLUS COPYRIGHT 1997 ACS

1994:184105 Document No. 120:144115 A gene encoding a chloroplast

**.omega.3 fatty acid desaturase**

complements alterations in **fatty acid**

**desaturation** and chloroplast copy number of the fad7

mutant of Arabidopsis thaliana. Iba, Koh; Gibson, Sue;

Nishitani, Takumi; Fure, Takashi; Hishinuma, Mitsuo; Arndel,

Vincent; Haily, Susanne; Scaevallie, Chris (Fac. Sci., Kyushu Univ.,

Fukuoka, 812, Japan). J. Biol. Chem., 269(3), 24399-105 (English)

1994. CODEN: JBSCH3. ISSN: 0021-9758.

AB **Mutations** at the fad7 locus of A. thaliana (previously

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called *fadD*) cause decreased **desatn.** of dienoic **fatty acids** in chloroplast lipids in plants grown at elevated temps. This suggested that the *fad7* locus encodes a chloroplast  $\omega$ -3 desaturase that catalyzes the **desatn.** of lipid-linked 18:2 and 16:3 fatty acids. In order to clone the *fad7* gene, it was first genetically mapped relative to the flanking RFLP markers 1647 and 2438A on chromosome 3, and yeast artificial chromosomes covering the locus were identified. A putative desaturase cDNA clone that was isolated by low stringency heterologous probing with a cDNA for an endoplasmic reticulum-localized  $\omega$ -3 desaturase (*fa3*) hybridized to the yeast artificial chromosomes and could not be resolved from the locus by RFLP mapping. Expression of the cDNA in transgenic *fad7* **mutant** plants resulted in restoration of wild-type fatty acid compn. and suppression of a previously obsd. effect of the *fad7* **mutation** in chloroplast n.a. indicating genetic complementation. The structural gene contained seven introns within a coding sequence of 1333 base pairs, which encodes a 446-amino acid polypeptide of 51,172 daltons. The N-terminal region of the *fad7* gene product contained a consensus chloroplast transit peptide. Except for the N-terminal domain, the deduced amino acid sequence of the *fad7* gene product had high homol. to the *fa3* gene product, indicating that *fad7* encodes an  $\omega$ -3 desaturase and that the two genes arose from a common ancestral gene. There was no apparent effect of growth temp. on the steady-state levels of *fad7* mRNA in wild-type plants.

- CC 3-3 (Biochemical Genetics  
Section cross-reference(s) : 7, 11
- ST **fatty acid desaturase** gene: sequence  
Arabidopsis; mapping sequence gene *fad7* Arabidopsis
- IT Arabidopsis thaliana  
(**fatty acid desaturase** gene *fad7*  
of, isolation and sequence and mapping of
- IT Chloroplast  
(**fatty acid desaturase** of,  
Arabidopsis thaliana gene for, isolation and sequence and mapping  
of)
- IT Deoxyribonucleic acid sequences  
of **fatty acid desaturase** gene  
*fad7*, of Arabidopsis thaliana)
- IT Protein sequences  
of **fatty acid desaturase**, of  
Arabidopsis thaliana)
- IT Genetic mapping  
of fatty desaturase gene *fad7*, on Arabidopsis thaliana  
chromosome 3)
- IT Gene, plant  
EL: BIOL (Biological study)  
of *fad7*, for **fatty acid desaturase**,  
of Arabidopsis thaliana, isolation and sequence and mapping of)
- IT Chromosome  
(Arabidopsis thaliana), **fatty acid  
desaturase** gene *fad7* mapping)
- IT Peptides, biological studies  
EL: BIOL (Biological study)  
(transit, in **fatty acid desaturase**,  
of Arabidopsis thaliana)
- IT 149955-97-5,  $\omega$ -3-Fatty acid  
**desaturase** (Arabidopsis thaliana clone g4)  
EL: PEP (Properties)  
(amino acid sequence of)
- IT 153608-91-4, GenBank S66769  
EL: PEP (Properties)  
(nucleotide sequence of and mapping of)

L24 ANSWER 16 OF 19 HCAPLUS COPYRIGHT 1997 ACS

1994:47043 Document No. 129:47043 Cloning of higher plant omega.-3

**fatty acid desaturases.** Yadav, Narendra

S.; Wierzbicki, Anna; Aspartier, Mary; Caster, Cheryl S.; Perez-Grau, Luis; Kinney, Anthony J.; Hitz, William D.; Booth, J. Russell, Jr.; Schweper, Bruce; et al. (Exp. Stn., E. I. duPont de Nemours and Co., Wilmington, DE, 1986-1992, USA). Plant Physiol., 103(2), 167-76 (English) 1993. CODEN: PLPRAY. ISSN: 0032-1839.

AB *Arabidopsis thaliana* T-DNA transformants were screened for

**mutations** affecting seed fatty acid compn. A **mutant**

line was found with reduced levels of linolenic acid (18:3) due to a T-DNA insertion. Genomic DNA flanking the T-DNA insertion was used to obtain an *Arabidopsis* cDNA that encodes a polypeptide identified as a microsomal omega.-3 **fatty acid**

**desaturase** by its complementation of the **mutation**.

Anal. of lipid content in transgenic tissues demonstrated that this enzyme is limiting for 18:3 prodn. in *Arabidopsis* seeds and carrot hairy roots. This cDNA was used to isolate a related *Arabidopsis* cDNA, whose mRNA is accumulated to a much higher level in leaf tissue relative to root tissue. This related cDNA encodes a protein that is a homolog of the microsomal desaturase but has an N-terminal extension deduced to be a transit peptide, and its gene maps to a position consistent with that of the *Arabidopsis* fadD locus, which controls plastid omega.-3 levatin. These *Arabidopsis* cDNAs were used as hybridization probes to isolate cDNAs encoding homologous proteins from developing seeds of soybean and rapeseed. The high degree of sequence similarity between these sequences suggests that the omega.-3 desaturase use a common enzyme mechanism.

CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 7, 11

ST sequence plant **fatty acid desaturase**

gene; *Arabidopsis* **fatty acid desaturase**

gene fadD; soybean **fatty acid desaturase**

gene fadD; rapeseed **fatty acid**

**desaturase** gene fadD

IT Gene, plant

RL: BIOL (Biological study)

fadD, for **fatty acid desaturase** of

*Arabidopsis* and soybean and rapeseed, sequence of)

IT *Arabidopsis thaliana*

*Brassica napus*

Soybean

(**fatty acid desaturases** of

mitochondria and chloroplast of, sequence of genes for)

IT Seed

linolenic acid levels in *Arabidopsis thaliana*, cloning of

**fatty acid desaturase** gene affecting)

IT Protein sequences

of **fatty acid desaturase**, of

soybean and rapeseed and *Arabidopsis* microsomal and chloroplast)

IT Deoxyribonucleic acid sequences

complementary, for **fatty acid**

**desaturase**, of soybean and rapeseed and *Arabidopsis*

microsomal and chloroplast)

IT Gene, plant

RL: BIOL (Biological study)

fadD, for **fatty acid desaturase** of

*Arabidopsis* and soybean and rapeseed chloroplast, sequence of)

IT 463-40-1, Linolenic acid

RL: PRP (Properties)

(*Arabidopsis thaliana* seeds with reduced levels of, cloning of

**fatty acid desaturase** gene causing)

IT 149955-96-4, omega.-3 **Fatty acid**

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**desaturase** (Arabidopsis thaliana clone CFI gene fad3)  
 149955-97-5, .omega.-3 **Fatty acid**  
**desaturase** (Arabidopsis thaliana chloroplast clone CFD gene  
 fadD precursor) 149956-00-3, .omega.-3 **Fatty**  
**acid desaturase** (Glycine max clone GMD gene fad3)  
 149956-01-4, .omega.-3 **Fatty acid**  
**desaturase** (Glycine max chloroplast clone GMD gene fadD)  
 152208-01-0, .omega.-3 **Fatty acid**  
**desaturase** (Brassica napus chloroplast clone BND gene fadD  
 precursor) 152208-02-1, .omega.-3 **Fatty**  
**acid desaturase** (Brassica napus clone BM2 gene  
 fad3)

HL: PEP (Properties)  
 (amino acid sequence of)

IT 149955-99-5 149955-99-3 149955-99-2 149955-93-1 151497-59-5  
 151497-60-3

HL: BICL (Biological study); PEP (Properties)  
 (nucleotide sequence of)

L24 ANSWER 17 OF 19 HCAPLUS COPYRIGHT 1997 ACS

1993:418436 Document No. 119:318623 Map-based cloning of a gene  
 controlling omega-3 **fatty acid**

**desaturation** in Arabidopsis. Arendel, Vincent; Lemieux,  
 Bertrand; Hwang, Inwon; Gibson, Sue; Goodman, Howard H.;  
 Somerville, Chris R. (Plant Res. Lab., Michigan State Univ., East  
 Lansing, MI, 48824-1312, USA). Science (Washington, D. C., 1983-),  
 258(5096), 1993-5 (English) 1993. CODEN: SCIEAS. ISSN: 0036-8075.

AB A gene from the flowering plant Arabidopsis thaliana that encodes an  
 .omega.3 desaturase was cloned on the basis of the genetic map  
 position of a **mutation** affecting membrane and storage  
 lipid fatty acid compn. Yeast artificial chromosomes covering the  
 genetic locus were identified and used to probe a Brassica napus  
 seed cDNA library. A B. napus cDNA clone for the desaturase was  
 identified and introduced into roots of both wild-type and  
 mutant A. thaliana plants by Ti plasmid-mediated  
 transformation. Transgenic tissues of both **mutant** and  
 wild-type plants had significantly increased amts. of the  
**fatty acid** produced by this **desaturase**.

CC 3-3 (Biochemical Genetics)  
 Section cross-reference(s) : 1, 11

ST omega3 desaturase gene mapping Arabidopsis; cDNA omega3 desaturase  
 sequence cloning Brassica

IT Arabidopsis thaliana  
 (gene fad3 for .omega.3 linoleate desaturase of, mapping of)

IT Genetic mapping  
 (of gene fad3 for .omega.3 linoleate desaturase, of Arabidopsis  
 thaliana)

IT Protein sequences  
 (of .omega.3 linoleate desaturase, of Brassica napus)

IT Root  
 (transformation of, of Arabidopsis thaliana, by .omega.3  
 linoleate desaturase cDNA of Brassica napus)

IT Brassica napus  
 (.omega.3 linoleate desaturase cDNA of, sequence and cloning in  
 Arabidopsis thaliana of)

IT Gene, plant  
 HL: BICL (Biological study)  
 (fad3, for .omega.3 linoleate desaturase, of Arabidopsis  
 thaliana, mapping and complementation of)

IT Deoxyribonucleic acid sequences  
 (complementary, for .omega.3 linoleate desaturase, of Brassica  
 napus)

IT Transformation, genetic  
 (transgenesis, of Arabidopsis thaliana roots, by .omega.3

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- linoleate desaturase cDNA of *Brassica napus*)
- IT Chromosome  
*Arabidopsis thaliana* L, gene fad1 for omega.3 linoleate  
 desaturase mapping on)
- IT **148814-49-7**  
 RL: BAC (Biological activity or effector, except adverse); PRP  
 (Properties); BIOL (Biological study);  
 (amino acid sequence of, complete)
- IT 17213-43-6  
 RL: FORM (Formation, nonpreparative)  
 (formation of, by transgenic *Arabidopsis thaliana* expressing  
*Brassica napus* omega.3 linoleate desaturase cDNA)
- IT 148814-49-8, GenBank L01411  
 RL: BIOL (Biological study); PRP (Properties)  
 (nucleotide sequence of)
- L24 ANSWER 13 OF 13 HEADLINE COPYRIGHT 1997 ACS  
 1993:133176 Document No. 119:133176 **Fatty acid  
 desaturase** genes from plants and their use in altering fatty  
 acid composition of plant oils. Browse, John; Grau, Luis Perez;  
Pinney, Anthony J.; Pierre, John W., Jr.; Wierzbicki, Anna M.;  
Yakov, Narendra S. (du Pont de Nemours, E. I., and Co., USA). PCT  
 Int. Appl. WO 9311245 A1 930610, 167 pp. DESIGNATED STATES: W: AU,  
 BR, CA, JP, RU, UA, US; BW: AI, BE, CH, DE, DK, ES, FR, GB, GR, IE,  
 IT, LU, MC, NL, FI, SE. (English). CODEN: PIXXD2. APPLICATION: WO  
 93-0310-4 921313. PRIORITY: US 91-04289 911214.
- AB Plasmid and mitochondrial **delta-15** desaturase cDNAs  
 of *Arabidopsis thaliana*, *Brassica napus*, and *Glycine max* are cloned  
 and sequenced. The effect on 18:2 and 18:3 content of expression of  
 antisense **delta-15** desaturase cDNA in *B. napus*  
 and *G. max* was examd. Use of the cloned cDNA for RFLP anal. and  
 plant breeding was explored.
- IC 1CM C110613-5;  
 1CS C110613-33; C113001-11; C130011-63
- CC 3-2 (Biochemical Genetics)  
 Section cross-reference(s): 11, 17
- ST **fatty acid desaturase** cDNA plant  
 sequence; *Arabidopsis* delta15 desaturase cDNA sequence; *Brassica*  
 delta15 desaturase cDNA sequence; *Glycine* delta15 desaturase cDNA  
 sequence; oil glyceridic plant unsatd fatty acid; RFLP plant  
 breeding desaturase cDNA
- IT Plant breeding and selection  
 RFLP anal. in plant **.DELTA.-15**  
**fatty acid/glycerolipid desaturase**  
 (cDNA for)
- IT Gene, plant  
 RL: BIOL (Biological study)  
 (for **.DELTA.-15 fatty acid**  
 glycerolipid **desaturase** of *Arabidopsis thaliana* and  
*Brassica napus* and *Glycine max*)
- IT Protein sequences  
 of **.DELTA.-15 fatty acid**  
 glycerolipid **desaturase** of *Arabidopsis thaliana* and  
*Brassica napus* and *Glycine max*.
- IT Plant  
 (oil-producing, alteration of linolenic acid content of  
 transgenic, cloning of plant **.DELTA.-15**  
 desaturase cDNA in relation to)
- IT *Arabidopsis thaliana*  
*Brassica napus*  
*Cocoa* (*Theobroma cacao*)  
 Corn  
 Cotton  
 Peanut

Safflower  
Soybean  
Sunflower

(plant **.DELTA.-15 fatty**

**acid/glycerolipid desaturase** cDNA expression

in, for alteration of linolenic acid content of oil)

IT Fat and Glyceridic oils

RL: BIOL (Biological study)

with altered linolenic acid content, transgenic plants

producing, cloning of plant **.DELTA.-15**

**desaturase** cDNA in relation to

IT Deoxyribonucleic acid sequences

complementary, for **.DELTA.-15 fatty**

**acid/glycerolipid desaturase** of *Arabidopsis*

*thaliana* and *Brassica napus* and *Glycine max*)

IT Genetic polymorphism

restriction fragment length, of plant genomes, plant

**.DELTA.-15 fatty acid**

**glycerolipid desaturase** cDNA for anal. of

IT 149955-96-4, **.DELTA.-15 Desaturase**

(*Arabidopsis thaliana* clone pCF3; 149955-97-5,

**.DELTA.-15 Fatty acid**

**desaturase** (*Arabidopsis thaliana* clone pACE2; plastid)

149955-98-6, **.DELTA.-15 Glycerolipid**

**desaturase** (*Brassica napus* clone pBNSF3-2 microsomal)

149955-99-7, **.DELTA.-15 Glycerolipid**

**desaturase** (*Brassica napus* clone pBNSF4-2 plastid)

149956-00-3, **.DELTA.-15 Desaturase**

(*Glycine max* clone pXF1 microsomal) 149956-01-4,

**.DELTA.-15 desaturase** (*Glycine max* clone

pSFD-118bwp plastid) 149956-02-5, **.DELTA.-**

**15 desaturase** fragment (*Zea mays* clone pCF30,

149956-03-6, **.DELTA.-15 desaturase**

fragments (*Arabidopsis thaliana* clone pFack-2 plastid)

RL: PEP (Properties)

amino acid sequence of

IT 149955-8-3, DNA (*Arabidopsis thaliana* clone pCF3 **.DELTA.-**

**15 desaturase** cDNA and flanks) 149955-91-3, DNA

(*Arabidopsis thaliana* clone pACE2-2 plastid **fatty**

**acid .DELTA.-15 desaturase**

cDNA and flanks) 149955-91-3, DNA (*Brassica napus* clone pBNSF3-2

microsomal **.DELTA.-15 glycerolipid desaturase**

cDNA and flanks) 149955-92-1, DNA (*Glycine max* clone pXF1

microsomal **.DELTA.-15 desaturase** cDNA and

flanks) 149955-93-1, DNA (*Glycine max* clone pSFD-118bwp plastid

**.DELTA.-15 desaturase** cDNA and flanks)

149955-94-2, DNA (*Zea mays* clone pCF30 **.DELTA.-15**

**desaturase** cDNA) 149955-94-3, DNA (*Arabidopsis thaliana* clone

pFack-2 plastid **.DELTA.-15 desaturase** cDNA)

RL: BIOL (Biological study); PEP (Properties)

nucleotide sequence of, use in RFLP anal. and in transgenic

plants for alteration of fatty acid content of oils of)

IT 46-46-1, Linolenic acid

RL: PEP (Properties)

transgenic plants producing oil with altered levels of, cloning

of plant **.DELTA.-15 desaturase** cDNA in

relation to)

L24 ANSWER 13 OF 15 HTAPLUS COPYRIGHT 1997 ACS

1991:1874 Document No. 114:1-574 The OLE1 gene of *Saccharomyces*

*cerevisiae* encodes the **.DELTA.9 fatty acid**

**desaturase** and can be functionally replaced by the rat

stearoyl-CoA desaturase gene. Stuke, Joseph E.; McDonough,

Virginia M.; Martin, Charles E. (Nelson Biol. Lab., Rutgers, State

KATHLEEN FULLER BT/LIBRARY 308-4290

Univ., Piscataway, NJ, 08855-1059, USA). J. Biol. Chem., 265(33), 20144-9 (English) 1990. CODEN: JBCHA3. ISSN: 0021-9258.

AB Strains of *S. cerevisiae* bearing the *ole1* **mutation** are defective in unsatd. fatty acid (UFA) synthesis and require UFAs for growth. A previously isolated yeast genomic fragment complementing the *ole1* **mutation** was sequenced and found to encode the **DELTA-9 fatty acid desaturase** enzyme by comparison of primary amino acid sequence to the rat liver stearyl-CoA desaturase. The *OLE1* structural gene encodes a protein of 513 amino acids (2.1 hydrophobic) having an approx. mol. mass of 55.4 kDa. A 357-amino acid internal region of the yeast open reading frame aligns with and shows 88% identity and 63% similarity to the rat liver stearyl-CoA desaturase protein. This comparison disclosed 3 short regions of high consecutive amino acid identity (70%) including one 11 of 12 perfect residue match. The predicted yeast enzyme contains 4 potential membrane-spanning regions and several shorter hydrophobic regions that align exactly with similar sequences in the rat liver protein. An *ole1* gene-disrupted yeast strain was transformed with a yeast-rat chimeric gene consisting of the promoter region and N-terminal 27 codons of *OLE1* fused to the rat desaturase coding sequence. Fusion gene transformants displayed near equiv. growth rates and modest lipid compn. changes relative to wild-type yeast control implying a significant conservation of **DELTA-9** desaturase tertiary structure and efficient interaction between the rat desaturase and yeast cytochrome b5.

CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 7

ST **fatty acid desaturase** gene sequence

*Saccharomyces*; gene *OLE1* sequence *Saccharomyces*

IT *Saccharomyces cerevisiae*

(**fatty acid desaturase** gene *OLE1*)

cf, nucleotide and encoded peptide sequences of)

IT Endoplasmic reticulum

(**fatty acid desaturase** insertion

into cell membrane of, of *Saccharomyces cerevisiae*)

IT Protein sequences

(of **fatty acid desaturase**, of

*Saccharomyces cerevisiae*, complete

IT Fatty acids, biological studies

Lipids, biological studies

EL: BIOC (Biological study)

(of transformed *Saccharomyces cerevisiae* contg. **fatty**

**acid desaturase** gene

IT Complementation, genetic

stearyl CoA desaturase gene in, of yeast cells contg.

**mutant fatty acid desaturase**

genes)

IT Fat

stearyl CoA desaturase gene of, in complementation of

*Saccharomyces cerevisiae* contg. **mutant fatty**

**acid desaturase** gene)

IT Long-chain fatty acid sequences

acyl CoA desaturase-specifying, of *Saccharomyces cerevisiae*,

(complete)

IT Fatty acids, biological studies

EL: BIOC (Biological study)

unsatd., of transformed *Saccharomyces cerevisiae* contg.

**fatty acid desaturase** gene)

IT Gene and genetic element, microbial

EL: BIOC (Biological study)

*OLE1*, for **fatty acid desaturase**,

of *Saccharomyces cerevisiae*, nucleotide and encoded peptide

sequences of)

.IT 131198-85-1  
 FL: PRP (Properties)  
 (amino acid sequence of)  
 IT 3014-34-0, DELTA-9 Fatty acid  
 desaturase  
 FL: PRP (Properties)  
 gene for, of *Saccharomyces cerevisiae*, structure and  
 complementation anal. of)  
 IT 131198-85-9, Deoxyribonucleic acid (*Saccharomyces cerevisiae* gene  
 CLE1)  
 FL: BIOL (Biological study); PRP (Properties)  
 (nucleotide sequence of)  
 IT 57-11-3, Fatty acid 16:0, biological studies 57-11-4, Octadecanoic  
 acid, biological studies 112-50-1, 9-Octadecenoic acid (Z)-,  
 biological studies 573-49-2 544-63-1, Tetradecanoic acid,  
 biological studies  
 FL: BIOL (Biological study)  
 (of transformed *Saccharomyces cerevisiae* contg. fatty  
 acid desaturase gene)

=> sel hit rn 1-19

E1 THROUGH E36 ASSIGNED

=> file reg

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 SEL HIT RN 1-19

FILE 'REGISTRY' ENTERED AT 11:41:12 ON 18 DEC 1997

L25 16 S E1-E36

=> s 15 and 125

L26 36 L5 AND L25

=> d 126 sqide can

L26 ANSWER 1 OF 36 REGISTRY COPYRIGHT 1997 ACS  
 RN 197594-15-3 REGISTRY

KATHLEEN FULLER BT/LIBRARY 308-4290

• CN Desaturase, oleoyl coenzyme A (Petroselinum crispum clone ELI12)  
(CI) CA INDEX NAME

## OTHER NAMES:

GN GenBank U56374-derived protein GI 2101792

PS PROTEIN SEQUENCE

SeqL 383

```

SEQ      1 MDAAGGHSISIP PDKKTAASA LKRAPHEKEP ETIGILKKAI PAHCFQKSLV
      51 TSPRYLIQDL PMAYALFYVA TNYIDQILET PENYVAAWY IAVQGEVLTG
     101 AWVVEHCIEH DAFQYNNWIN DADGLTSSS LLYPYFSWKL SHREHHANTQ
      ==  ==
     151 SIENDEFTVP RPYNNIENYY ELNNPQGV LKWLTLIIG FPLYINENVS
     201 GKKYEFWTER YDREPLYSD EEREKLIUSD IAILAVIYDL YQLVLAQGEA
      ==  ==
     251 WYFQVYQGEPL LVYAGWFYLY TLNHTHPSL PYDSTEWIW LEGALCTVDA
     301 DYHILNTER DADARVCHH LPSHIPPYRG LESTFAMHFI LGEYTPQDGT
      ==  ==
     351 PLKAMYREH PNYIYVENDE GETEGYWEY NKF
  
```

HITS AT: 106-110, 141-146, 113-114, 116-320

MF Unspecified

CI MAN

SR CA

LC STM Files: CA, CAPLUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 1.7:31084

and 1.7:31084 can 2-3.

L26 ANSWER 1 OF 36 REGISTRY COPYRIGHT 1997 ACS

EN 197594-14-2 REGISTRY

CN Desaturase, fatty acid omega.3- Petroselinum crispum clone 15-1)  
(CI) CA INDEX NAME

## OTHER NAMES:

GN GenBank U56374-derived protein GI 1789096

PS PROTEIN SEQUENCE

SeqL 438

```

SEQ      1 MAAWVIFQCG IRLIFRIYAK IRGQAZQFNS ENEVENLEFL DENVKISHTG
      51 CRHWGLQVSV LMSVFSVNEE EEFPECLNEE ENKEIPGAAP PEKESINFAA
     101 IPYKOWYQDF VEMSYVIED VLIYFQAVA ASFVNKAWW PLYWIAQGTG
     151 PWALPVLQHD CGHQSFSIDA FLNIVGHIL ESSLVFPYHG WELSHETHHQ
      ==  ==
     201 DEGHVENNES WHEIIEKLEN CLMLTKEER ETLEFPMLAY PFYLWGRSPG
      ==  ==
     251 KGGSHYTFSS FLEVPNERKL VITVTQWTA MAALLVGLDF VMGPVNMML
     301 YGIPYWIPEVH WLPVITYLHH EGHDELEPWY EKEWSYLFQ GLTTLQDYG
      ==  ==
     351 WINNIHSDIG ENEHRLPPQ IPHYRLIAT EAQKIVEGQY YREPHEGQPV
      ==  ==
     401 PFHLATLWK FPEDEHFSQ TGIQVYVYQAH PETAPTQK
  
```

HITS AT: 119-161, 19-112, 319-323, 362-366

MF Unspecified

CI MAN

SR CA

LC STM Files: CA, CAPLUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 1.7:31084

L26 ANSWER 3 OF 36 REGISTRY COPYRIGHT 1997 ACS

KATHLEEN FULLER BT/LIBRARY 308-4290

EN 196217-80-8 REGISTRY  
 CN 384-721-Desaturase, oleate (Corylus avellana clone I) (9CI) (CA  
 INDEX NAME)  
 PS PROTEIN SEQUENCE  
 SQL 338

SEQ 1 QEQLLRSPSY VVYDLSLAPL EYYIATSYFH LIPHPLELYA WSIYWALQGC  
 = == =  
 51 LTGVAWVIAH EDSHHAESDY QWYDMVGLT LKALNPYF SWKISHCRHH  
 == == ==  
 101 SUTGSLDRDE VVYPPFESH EWEAEYFENP PGEVLTLIT LTGWFYLYA  
 151 LKNSRPPYD PASHYDQYQ LYNIEKQQL EWDAGVFAT TTYLYAAMS  
 201 ERLAWLPIY GMLLLVNGE LYLITVQRT HPALPHYDGS EWDWLEGALA  
 251 TAQRDYSKLN EYFRIIDTH VAKHLESTIP HYRAMEATRA LKSLCKYYQ  
 == == ==  
 301 EDDTPYFYN WKEAECLAY EWDGAPNES VEWYQSEL

HITS AT: 31-64, 65-66, 66-100, 100-204

MF Unspecified

CI MAN

SE CA

SC STM Files: CA, CAPUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPUS (1967 TO DATE)

REFERENCE 1: 197:15-443

1.6 ANSWER 4 OF 30 REGISTRY COPYRIGHT 1997 ACS

EN 196217-78-4 REGISTRY

CN Desaturase, oleate (Corylus avellana clone N2 gene PAD2-N) (9CI)  
 (CA INDEX NAME)

PS PROTEIN SEQUENCE

SQL 382

SEQ 1 DGAGSRMFAT HNEEFQTEI QWANTHDEF TLGQLKFAVP PICEQFSEL  
 51 SPSTYVVIS LAFYFYIAT YFHLPHSL CYLAWNTYWA LQGLLTGVW  
 == == ==  
 101 VIANECGHH AFSDYQWLDD TVGLIFHSFL LVPYFQWYYS HARRHHSNTGS  
 == == ==  
 151 LADGTFNTH KSHHWESKY EHNPPGNIT LITITLQWP LYLALVSGH  
 201 PYDEFACHD EYGLYSNEP EQLFYSIAG VEATYVLLY AMHKGLAWL  
 251 VYVDSHLLT YGFIATLTY LGTHPAIEH YNISEW WLR GALATADEY  
 301 GHNTPFHHI LTHVAHIE STNPHYAME ATFAIKCIG KTYQFLGTEV  
 == == ==  
 351 YVAVWEBAE CLYVESRCA EFWQVFWYQS EL

HITS AT: 35-66, 66-100, 100-144, 144-213

MF Unspecified

CI MAN

SE CA

SC STM Files: CA, CAPUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPUS (1967 TO DATE)

REFERENCE 1: 197:15-443

1.6 ANSWER 5 OF 30 REGISTRY COPYRIGHT 1997 ACS

EN 192889-81-9 REGISTRY

CN Desaturase, oleoylcothar (Brassica napus clone Q50 isoenzyme F)  
 (9CI) (CA INDEX NAME)

PS PROTEIN SEQUENCE

SQL 384

SEQ 1 DGAGSRMFAT HNEEFQTEI QWANTHDEF TLGQLKFAVP PICEQFSEL  
 51 RSELYLWLDI LIASCFYVA TTYEPLLEP LSYFAWPLYW AQDGCYLTGV  
 101 WVIANECGHH AFSDYQWLDD TVGLIFHSFL LVPYFQWYYS HARRHHSNTGS  
 KATHLEEN FULLER BT LIBRARY 300-4290

```
=====
151 LERDEVEFVPE HKSDIKWYGH YHNNPLGRIV MLTVQFTLQW PLYLAFNVSG
201 RPYDGGGEACH PHHNAPIYND RERLQIYISD AGILAVCYGL YRYAAMQGVA
251 SHVCFYGVPL LITNGLVLI TYLQHTHPSL PHYDSSEWQW LEGALATVDE
301 IYQILNKVPH NITLTHVAHH LESTMPHYHA MEATEAIKFI LGEYYQIHGT
=====
```

351 IYKAMWSEA HECIYVEPDE QGEMFGVFWY INEL

HITS AT: 100-100, 141-140, 316-320

MF Unspecified

CI MAN

SR CA

LC STM Files: CA, CAPLUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 107:135000

126 ANSWER 6 OF 10 REGISTRY COPYRIGHT 1997 ACS

EN 192889-79-5 REGISTRY

CN Desaturase, oleoyl-coithin (Brassica napus strain Westar; asoenzyme F) (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE

SQL 384

```
SEQ 1 MGVGGKMAVS HIFHSEBTDI IKRNICHTSI PTUGELFKAI PSHCFEESIF
51 RPSFYLIWDI IACQFYFNA TTYHLLERH LSYFAWELNW AQQGCNLTGV
101 WYLAHNDVHH APTTYQWLDI TVGLIHSEI LVYFQWYKYS HSRHHNTTGS
=====
151 LERDEVEFVPE HKSDIKWYGH YHNNPLGRIV MLTVQFTLQW PLYLAFNVSG
101 RPYDGGGEACH PHHNAPIYND RERLQIYISD AGILAVCYGL YRYAAMQGVA
151 SHVCFYGVPL LITNGLVLI TYLQHTHPSL PHYDSSEWQW LEGALATVDE
101 IYQILNKVPH NITLTHVAHH LESTMPHYHA MEATEAIKFI LGEYYQIHGT
=====
```

351 IYKAMWSEA HECIYVEPDE QGEMFGVFWY INEL

HITS AT: 100-100, 141-140, 316-320

MF Unspecified

CI MAN

SR CA

LC STM Files: CA, CAPLUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 107:135000

126 ANSWER 7 OF 10 REGISTRY COPYRIGHT 1997 ACS

EN 192889-77-3 REGISTRY

CN Desaturase, oleoyl-coithin (Brassica napus clone IMC129; asoenzyme D) (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE

SQL 384

NTE

type	location	description
uncommon	A13-69	-

```
SEQ 1 MGVGGKMAVS HIFHSEBTDI IKRNICHTSI PTUGELFKAI PSHCFEESIF
51 RPSFYLIWDI IACQFYFNA TTYHLLERH LSYFAWELNW AQQGCNLTGV
101 WYLAHNDVHH APTTYQWLDI TVGLIHSEI LVYFQWYKYS HSRHHNTTGS
=====
151 LERDEVEFVPE HKSDIKWYGH YHNNPLGRIV MLTVQFTLQW PLYLAFNVSG
201 RPYDGGGEACH PHHNAPIYND RERLQIYISD AGILAVCYGL YRYAAMQGVA
251 SHVCFYGVPL LITNGLVLI TYLQHTHPSL PHYDSSEWQW LEGALATVDE
```

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301 DYGILNKVFH NITDTHVAHH PEETMPHYHA NEATKAIRPI LGEYYQFDST

=====

51 PVVKAMWSEA KECIVVERPDR QGEEKGVFWY NNEL

HITS AT: 106-109, 141-143, 316-320

MF Unspecified

CI MAN

CE CA

CC STM Files: CA, CAPLUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 127:135-136

1.6 ANSWER 4 OF 36 REGISTRY COPYRIGHT 1997 ACS

EN 192889-75-1 REGISTRY

CH Desaturase, oleoyl-coA: (Bovine strain Westar isoenzyme  
D) (9CI) (CA INDEX NAME)

FI PROTEIN SEQUENCE

SQL 384

NTE

Type	Location	Description
Uncommon	Asa-65	-

SEQ 1 MGAGGAMWVS PSMKSEEDT LKATPCSTTP FTUGELKKAI PRCTFPSIP  
51 KSPSYLWDI LKACFYWA TTPFLIPHP LSYFAWPIW ACQGCVLTSV  
101 WUTAKGCHH APEDQWLDL TQGLIFSEL LVEYFHWYS HPSHNTGS  
=====

151 LEEDEVTYK PPSIDWYOK YLLEPLQRTV MLTVQFELGW PLYLAFNVSG  
301 RPYGCGPCH PHHAPYND EELIQYISD AGILAWCYGL FRYAACQGVA  
451 SINTYCGPL LQVGHVAM TYQHTHPSL PHYSSEWVW FEGALAIQDS  
601 DYGILNKVFH NITDTHVAHH PEETMPHYHA NEATKAIRPI LGEYYQFDST  
=====

51 PVVKAMWSEA KECIVVERPDR QGEEKGVFWY NNEL

HITS AT: 106-109, 141-143, 316-320

MF Unspecified

CI MAN

CE CA

CC STM Files: CA, CAPLUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 127:135-136

1.6 ANSWER 4 OF 36 REGISTRY COPYRIGHT 1997 ACS

EN 186208-06-0 REGISTRY

CH Desaturase, DELTA-4-Fatty acid (Pichia angusta) (9CI) (CA INDEX  
NAME)

FI PROTEIN SEQUENCE

SQL 451

SEQ 1 MGRKSHNTVT AGRKEDSWA NMLAPDELEK NPYLQFHS EQPWTWINWH  
51 KHNWVNFIL VNAVFAQIL STFWVPLKLE TPTAVILNC FGGISITAGY  
101 HARWANRAYD QHLFQKFFA LQVSAVSSG IHWGQHFV HERYIDTPD  
=====

151 PYDAKSGFWY SHMGMLNP NPKYKARADL SDLLQWVVR VQRRHYLLM  
301 VVNASLPPAV LCHYLNDFW GGFYACLE AVYIQQATEC VNSLAHWIGE  
451 QPFDGSETPR DQVICALATF GQYHNFHEE FWDYRNALK WYQYDPTKVV  
=====

301 IYLLSEYGLA YULKEFSQNA IDQILQQQQ KPDDEMRKL NWGPQLSELP  
351 VWDKSTFFER AKDQGLVII SLVHDVANT LTERPGQAL LKTSFGKDAT  
401 MAFNGGYAH SNAAHNLIAT MKVAVIRKGG ANQDTFAQL RYLAKENKK

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451 E

HITS AT: 138-142, 275-279

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 116:113911

126 ANSWER 11 OF 36 REGISTRY COPYRIGHT 1991 ACS

RN 180583-92-0 REGISTRY

CN Desaturase, linoleate (Boraginaceae officinalis) (CAI) (CA INDEX NAME)

PS PROTEIN SEQUENCE

SQL 448

```

SEQ      1 MAAQIKKQIT SDLEENHDKS EDWISIQQK AYVSDWVMD HPGGSFPLKS
      51 LAGQNTDQAF VAFHASTWK NIDHEFTGYV LKDYVSSENS KDYRKLVFEE
     101 SPMGINTKRS RIMEATLOFI AMLFAMSVYG VLECEGVLRH LFSGQINGFL
     151 WIQSWIGHD AGHYMVVDS ELNRKMGIFA ANCLSGISIG WKKWHHNAHE
      201 IACNHLNDE IDQNPFIWV SCFFPGSLIS HYTFRLTFD SLSPFVSQYQ
     251 HWTFYPIHMA AALNNYVQSL IMILTERNVS YRAQELIGEL VFSIWYPLIV
     301 SCLPRNGERI RYVIALSLVI GNQOVQPSIH HFSSEYVYCK PKGNWFERQK
     351 TDGTDIDIE RWNWPHRGS QFQIEHLEFP RIFECILRKI SPYVIELCKK
     401 HNLPHRYANE SEAMENLRT LKNTALQARD ITPPLPFIWV WEALHTG

```

HITS AT: 159-163, 196-199

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 100:289090

REFERENCE 2: 100:161500

126 ANSWER 11 OF 36 REGISTRY COPYRIGHT 1991 ACS

RN 175960-67-5 REGISTRY

CN Oxidase, lipoic acid (Arabidopsis thaliana clone pFL6101) (CAI) (CA INDEX NAME)

PS PROTEIN SEQUENCE

SQL 281

```

SEQ      1 MAADNAYLDQ FVDETSEYNE IVICHILEAI LWFPIPEFLQ TWLRHYLAGT
      51 LLYLISGFHW CFTTYFERIN VYLSKLAIFT IKAMEIQNEV AMEAMPWYTL
     101 LETVREHIE EGWYCEASI GRPWLYIVY YIAIYLVFE FGIYWNREEL
      151 HDIKPLKEL HATHNYNQ NLSPFACIA FRVLDGILQA VPEVIALFIV
      201 HIFETTHIL LEMALWAAN IEDMNGNIW PVIAGYHTI HHTTYKENYG
     251 HYTIWHEWF GGLRGLLEE DINKDSEKFA E

```

HITS AT: 147-151, 161-163, 203-207, 222-226, 231-232, 247-251

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:30905

L26 ANSWER 12 OF 26 REGISTRY COPYRIGHT 1997 ACS

EN 168613-13-6 REGISTRY

CU Desaturase, fatty acyl coenzyme A (Anacystis nidulans strain P2-SPc reduced) (9CI) (CA INDEX NAME)

OTHER NAMES:

CU Desaturase, acyl coenzyme A (Synecococcus strain PCC 6301)

EC PROTEIN SEQUENCE

SQL 278

SEQ 1 MTLAIRPRLA EEWPTALEMV AINIGALLAF LPANFNWPAV GVMVALITYIT  
 51 GQPGITLQWH ELISHASPEV EKWLEYVLVF CGTLAIQHGF IENIGLRRHH  
 =====  
 101 HHSIQEYDHI EECNNGELWS EPLWNIYEIE ARCEVDEFTF DIASDEMYEF  
 =====  
 151 EKKYPTQYQV LIAVLLYAWG EAWVGNWSE VVGIFARLV VVTHVTLVN  
 201 SATHPQETLS HETGQSTNG EWWALLAFGE GWHNNHAYQ YSARHCLQKW  
 =====  
 251 EFDLTWIND GIKKTLARK IETASPNH

HITS AT: 97-100, 103-107

MF Unspecified

CI MAH

SE CA

SC STM Files: CA, CAPLUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:30905

L26 ANSWER 13 OF 26 REGISTRY COPYRIGHT 1997 ACS

EN 163961-98-6 REGISTRY

CU Desaturase, fatty acid omega.6- Arabidopsis thaliana gene fad6) (9CI) (CA INDEX NAME)

EC PROTEIN SEQUENCE

SQL 418

SEQ 1 MASEIALQNF APTGPTQCLP EWPILAASSA EWPFGVYAVE PIDLLNGRT  
 51 HNEFECVAVV KFFIGCIKAV AATVAPPSAD SAFDFQLAE SYGFRIGED  
 101 LPEVYTHKTI MCLPPEVE IDLKLKLSV LNVICYTIG LFHIAKSPWY  
 151 LILPLAWWIG TAITGFFWIG HICAKKSESE NELVEDVCT LAFLEPVPY  
 =====  
 201 EWWFETLHGH HANTMLVHD TAWQUPPEE FETSPVMRKA IIPSYQIRP  
 =====  
 251 WSHARWQW HEMLEFFAS EVNEVKISLA CVFATLAVGW PLIVYVAGIL  
 301 GWWFELIHW LGHFPMTEF TMTHETAPHI PYPALDWWNA AQAQLNGIVH  
 =====  
 351 QDYSWIEL CHINVEIPE HISPRIPSYK LEAARFSEIQ NWCKYTILAT  
 =====  
 401 WNWELMPTIM TDHUYDE

HITS AT: 171-173, 107-111, 323-329, 367-371

MF Unspecified

CI MAH

SE CA

SC STM Files: CA, CAPLUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:38103

L26 ANSWER 14 OF 26 REGISTRY COPYRIGHT 1997 ACS

EN 161027-24-3 REGISTRY

CU Desaturase, fatty acid DELTA.15- (Synecococcus sp. PCC 6803 clone pbluescript/6.0-kbp gene desB) (9CI) (CA INDEX NAME)

KATHLEEN FULLER BT/LIBRARY 503-4290

## OTHER NAMES:

CN Omega-3 Desaturase (Synchocystis sp. PCC 6803 clone  
 phagescript/5.6-kbp gene desP  
 GI GenBank D00012-derived protein GI 1611333  
 CN Protein (Synchocystis strain PCC 6803 clone  
 csl368/1211: csl368/1211:25-cs0391 open reading frame sll1441  
 reduced:  
 EC PROTEIN SEQUENCE  
 SQL 359

SEQ 1 MELNLSQQT KIPYKRIEL PFTIQELENA IPADPEPSV VRSLGYFFLD  
 51 TGLIAGPYAL AYVNDWPTY STEWLIQGL FWCLEFVGHG CGHSSPSKSK  
 101 TLNNKIGHLS HTPIANETHG WRISHRTHHA NTGNIDIDES WYPVSEQKYN  
 151 QHAWYKLLR EYLPDIAYPI YLFFASNNQ GSHFMGSSPL FEPDEKAAVL  
 201 TSTFACAAAY ELGLLWQF CWLEELNFTV APYLVEVWVL ELVTELHETE  
 251 LNIPTYSND WYFPGALST IDRDYGFNH IHRDIGIHYA HRIFSNMFY  
 301 KLRKATEAK ILGYYRYS DEPIWQAPPY SYWACHEVEN QGSEVYYQSP  
 351 LGGGTQRRP

HITS AT: 13-14, 15-18, 24-26

MF Unspecified

CI NAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 13:70-111

REFERENCE 1: 12:11,284

126 ANSWER IS OF 3- REGISTERED COPYRIGHT 1997 ACS

EN 158651-91-3 REGISTER

CN Desaturase, fatty acid omega-3- (Arachidopsis thaliana clone DES1  
 plastic-associated isoenzyme) (EC: CA INDEX NAME)

## OTHER NAMES:

CN Desaturase, fatty acid omega-3- (Arachidopsis thaliana gene fad8)  
 EC PROTEIN SEQUENCE  
 SQL 435

SEQ 1 MASNNLECG ERLPFRYPR HTTSEASNY PTHFNEPLK EPEELLNSRY  
 51 QFYPTFMA LNWYLTTL QSPSEELTFE FPGALFFN LADIRAAIPK  
 101 EOWYFHWK DQYFTRMAI YFGLAAYAY FNIWLNPLY WPAQGTMEWA  
 151 LSVVGRICGH QFPCHEELN YVAGRLIRCS ILNPIHGWEI SRETHHQNG  
 201 EYNDSEWHF LPEAIYHLE KITQMERETI PEINLAYPFY LWNELSPKQGG  
 251 LHYHDCDGF LPEKHIVLT STACWTAMAA LINCNEVMG FIQELKLYGE  
 301 PEWIPATWLD EWTILHHGR EDKLEWYRCF EWNYLPSGLT TLDSDYWIN  
 351 NHHHCTHY LHHLPQPR YHIVEATEAA KPWIGHYYRE EKNSGRLPLH  
 401 LGGSMKME LQHEWDTGD VVYYEADPM NGORT

HITS AT: 16-16, 17-19, 316-320, 359-363

MF Unspecified

CI NAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

3 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 12:26-91

REFERENCE 2: 101:257500

REFERENCE 3: 101:249101

L26 ANSWER 16 OF 36 REGISTERED COPYRIGHT 1997 ACS

EN 158283-34-2 REGISTERED

CN Desaturase, oleoyl coenzyme A (castor-oil plant clone pRF137C-42 reduced) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN .delta.-11 Fatty acid desaturase (Ricinus communis clone pRF197C-42)

EW PROTEIN SEQUENCE

SQL 387

```
SEQ      1 MGGGSRMSTV ILSNSENKKG CSNHLERAPH TEPYTLGNL KFAIPPHCFE
      51 KSPVSSPSNF AYNPCISPLS YSIATNFFPY ISNPLSYVAW LUYWLFQGGI
     101 MGLWVICHG CCHHAPSEYQ LADDIVGLIV HSALLVPYFS WKYSHERHHS
      131 HIGLEHREKV FVPSSTHIS WYKYLNNPP GRULTLAATL LLGWPLYLAF
     101 NVGSEYDRA AWHYDYGPI PSNEERLQIY IADLCIFATT EVLYQATMAK
     151 GLAKVMEIYG VPCLVNIGEL VMITYLQSTH PALPEYSSSE WDWLRGAMVT
     201 VDEGCGELNH VERNIALTRY ARIEATVSH YHAMEATRAI KPMGEYYRY
      231 DGTFFYALW EEAECIAPVE IDECAPTQGV FWYRNKY
```

HITS AT: 108-115, 127-133, 213-220

NP Unspecified

CI MAM

SE CA

IC STM Files: CA, CAPLUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 4: 101:200000

L 6 ANSWER 17 OF 36 REGISTERED COPYRIGHT 1997 ACS

EN 158283-32-0 REGISTERED

CN Desaturase, oleoyl coenzyme A (castor-oil plant clone pFad1 2,4-amine acid fragment reduced) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN .delta.-11 Fatty acid desaturase (Ricinus communis clone pF2-1C)

EW PROTEIN SEQUENCE

SQL 224

```
SEQ      1 WYKARDGHH ANNYQLDD VVGHILHSL LUYEFSWHS HERHHNTGS
      51 LRESEVPEK FKNVETWYSK YLNNPPGRIM TIATVLELGW ELYLAENVSG
     101 KPYGAYCHY LDTGEITNDE ERIRIFISDA GVLAVTEGLY QLAIAFGIAW
     151 VVCTYCHLL VCKFLVHTI FLQSTHPALP HYDSSEKDWL EGALATVDED
     201 YGIINKVTHI LTLTQVAHHL PTHI
```

HITS AT: 5-9, 41-45

NP Unspecified

CI MAM

SE CA

IC STM Files: CA, CAPLUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 101:200000

L26 ANSWER 18 OF 36 REGISTERED COPYRIGHT 1997 ACS

EN 158283-30-8 REGISTERED

CN Desaturase, oleoyl coenzyme A (corn clone pFad21 reduced) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN .delta.-12 fatty acid desaturase (Zea mays clone pFad2#1)

KATHLEEN FULLER BT/LIBRARY 308-4290

FS PROTEIN SEQUENCE  
SQL 387

```
SEQ      1 MGAGSEMTTEK EREKDEQLAR ATGGAAMQES PVEKPFETLG QIKKAIPPHC
      51 FERSVNICTEY YVHOLNIAA ALLYFALAH I PALPSELYA AWPLYWIAQG
     101 CYSTGVWVIA HEDSHHAFSI YSLDDWVVL VLRSSLIWVY FSWHYCHRRH
      ==
     151 HSHIGSLERD ENFVPRFKEA LPWITIVYN NPAGEVTHIV VQLTDSWPLY
      ==
     201 LATNASRETY PREACHEDPY GPIYNDREBA QIFVSDAGV AVAFGLYKLA
     251 AAFKWWYR EYAPLLIVN AWLLITVYIQ HTHPELPHYD SSEWDWLRGA
     301 LATKRLGGI LKNEPRHITL THVARELPST MPRYAREAT KAIRPILGCV
      =====
     351 YHSDTIVAF ATWREAGECI YVEPELERSV FWNKKK
```

HITS AT: 111-111, 14-111, 311-326

MF Unspecified

CI MAN

SE CA

IC STD Files: CA, CAPUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPUS (1967 TO DATE)

REFERENCE 1: 1.1:1040

106 ANSWER 13 OF 36 REGISTRY COPYRIGHT 1997 ACS

EN 158283-28-4 REGISTRY

CN Desaturase, oleyl desaturase A (cytochrome clone pSF2-165F reduced)  
reduced (CA INDEX NAME)

OTHER NAMES:

CN Delta-12 Fatty acid desaturase (Glycine max clone pSF2-165K)

FS PROTEIN SEQUENCE

SQL 379

```
SEQ      1 MGAGSEMAEK EYQGHFIEE VNTTHPEYV GQIKKAIPPH CEQFSLIIEF
      51 SYTYICLFA FETIATTFY HLLQFESLI AWLYWVWLG CLIGVWVIA
     101 HEDGSHAFSP YQWDDWVVL THSTILVY FSWHSHRRH HSNTGSLERD
      =====
     151 EYEMKREKY VAWSEPHIN PLGAASLV TLTGWIMYL AFNVSGREYD
     201 SPASHYHNYA ELYNREELI IYWDVALES VYSLYEVAT LKGLVWLLCV
     251 YQVPLIING FVNTITYQH THFALFHYDS SEWDWLRGAL ATNREYGLI
     301 NTHPRHITIT HVAHLESTH PRYAREATN AIPILGEYV QEDDTFYPA
      =====
     351 LWRNARECIY VHEEGCTEP QVYWRNEY
```

HITS AT: 101-101, 127-111, 311-315

MF Unspecified

CI MAN

SE CA

IC STD Files: CA, CAPUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPUS (1967 TO DATE)

REFERENCE 1: 1.1:1040

106 ANSWER 20 OF 36 REGISTRY COPYRIGHT 1997 ACS

EN 158283-26-2 REGISTRY

CN Desaturase, oleyl desaturase A (Brassica napus clone pCF2-165D)  
reduced (CA INDEX NAME)

OTHER NAMES:

CN Delta-12 Fatty acid desaturase (Brassica napus clone pCF2-165D)

FS PROTEIN SEQUENCE

SQL 383

```
SEQ      1 MGAGGHIYC PPSKESSTON IKR/PCETTP ETGGELEKAL PPHCFERSIP
      51 RSPSHLIWDI LIASCFYYVA TTYFPLLNP LSYFAWLYW ACQGGVLTGV
      KATHLEEN FULLER BT/LIBRARY 308-4290
```

```

101 WVIAHECGHA AFSDYWLED TWELIHSSEL LVVYFSWYYS HRRHESNTGS
=====
151 LERDEVEVPR RSQTSSTGAS TSTTGRTVM LTVQFTLQWP LYLAENVSGR
201 PVTGSGACHF HENAPIYNER ERLQIYISDA GILAVCYGLL PYAAVQGVAS
301 MTCFLWPLL IVNGFLVLIT YLQSTHPSLP HYDSEWVWL EGALATVDRD
401 YGILNQSPRN ITCTEAAHHL ESTTHPHYAM EATKAIKIL GEYYQFDGTR
=====

```

401 WVKAMWBEAK ECIYVEPDEQ GEEFGVFWYN DEL

HITS AT: 131-133, 141-143, 315-317

MF Unspecified

CI MAN

SE CA

LC STM Files: CA, CAPUS

1 REFERENCED IN FILE CA (1967 TO DATE)

1 REFERENCED IN FILE CAPUS (1967 TO DATE)

REFERENCE 1: 1.1:1.6040

126 ANSWER 11 OF 36 REGISTRY COPYRIGHT 1967 ACS

EN **158283-24-0** REGISTRY

CM Desaturase, legyl coenzyme A (Arabidopsis thaliana clone p92103  
reduced) (40) (CA INDEX NAME)

OTHER NAMES:

CM Delta-12 fatty acid desaturase (Arabidopsis thaliana clone p92103)

CM Oleate desaturase (Arabidopsis thaliana clone pE2a gene FAD2)

PC PROTEIN SEQUENCE

SQL **383**

```

SEQ      1 MGAGGMPVYP TATPKSTET TETPKCKEP EKVGLPWAI EPHCFKESIP
101 RQFSYLISDI TACQFYVA EHYFSLRPQ EGYLAWPLYW AQCGNLTGI
101 WVIAHECGHA AFSDYWLED TWELIHSSEL LVVYFSWYYS HRRHESNTGS
=====
151 LERDEVEVPR RSQTSSTGAS TSTTGRTVM LTVQFTLQWP LYLAENVSGR
201 PVTGSGACHF HENAPIYNER ERLQIYISDA GILAVCYGLY PYAAVQGVAS
301 MTCFLWPLL IVNGFLVLIT YLQSTHPSLP HYDSEWVWL EGALATVDRD
401 YGILNQSPRN ITCTEAAHHL ESTTHPHYAM EATKAIKIL GEYYQFDGTR
=====

```

401 WVKAMWBEAK ECIYVEPDEQ GEEFGVFWYN DEL

HITS AT: 131-133, 141-143, 315-317

MF Unspecified

CI MAN

SE CA

LC STM Files: CA, CAPUS

1 REFERENCED IN FILE CA (1967 TO DATE)

1 REFERENCED IN FILE CAPUS (1967 TO DATE)

REFERENCE 1: 1.1:1.6040

REFERENCE 2: 1.1:1.1400

126 ANSWER 2 OF 36 REGISTRY COPYRIGHT 1967 ACS

EN **156532-36-4** REGISTRY

CM Desaturase, legyl coenzyme A (Synecococcus strain PCC 7102 gene desA  
reduced) (40) (CA INDEX NAME)

OTHER NAMES:

CM Delta 12 desaturase (Synecococcus PCC7102)

PC PROTEIN SEQUENCE

SQL **347**

```

SEQ      1 HAVVTVPESA TTHLEKHPNL ELALILDTLP RQVYEINPLK AWRVLELVA
101 AVVGCYALLA IAWYILLIV WELTGTTLTG EFWIGHQGH EEPSSKQWVN
=====
101 NLVGHLEFLP LIYFERSWRI LNNHHHKYTN NMEDNAWAP ETPELYDQSP
=====

```

151 AFIKAVYPAI RGFLWWLASV IHQLKLFILW FAFEGHQREQ VRFSALFVII  
 251 AGAIAFFPME YLIGVWGVVW FWIMFWLGYH FWISTFFLVH HTVPEIPFSY  
 351 RSKWHEATAQ LSATVHCDFP KWTEVLCHDI NVHVPHRLST GIPSYNLEKA

=====

351 YASIQWQWGE YVETHEWE LMKATEQCH LYDAENNYIS FAQHQR

HITS AT: 8-99, 112-116, 123-127

MF Unspecified

CI MAN

SR CA

LC STM Files: CA, CAPLUN, TOXLIB

1 REFERENCES IN FILE CA (1-67 TO DATE)

1 REFERENCES IN FILE CAPLUN (19-7 TO DATE)

REFERENCE 1: 1.0:12-1117

REFERENCE 1: 1.1:14-1

LIFE ANSWER 13 OF 16 REGISTRY COPYRIGHT 1993 ACS

EN 156532-35-3 REGISTRY

CH Desaturase, *Synchytrium* (Synchytrium strain PCC 6714 gene desA reduced) (CC1) (CA INDEX NAME)

OTHER NAMES:

CH Delta 12 desaturase *Synchytrium* PCC6714)

EC PROTEIN SEQUENCE

SQL 349

SEQ 1 MTATPPIAP TETSSNPRI IALCLKQDI KTIPECFEK KASHAWLEVL  
 51 ITLGIALGY AGIYLPWYQ LPPWIKWTST ALIGAPVCH DCHRSFAEK

101 RWNQNLVHI APAPLIYER SWELIGHHR DRINKLEVEN AWI PWEVEAF

151 QASPAIVLE VETAGCPAWW TGIPIHWGLK RPYLENPAER SRNEVILSIA

201 VVPIBAAVAF PALIITGVW GPVFWLMIW LYHFWNSTF TFWHTIHEI

251 RFPDAEPWA ABAQLNGTVH CTFPFWVEVL CHFINVHIFH ELVAIFSYN

=====

351 IIAHANIPO NWQFLYFET FVWGLMQQIS GQCHLYIPN CYETESSIK

HITS AT: 8-99, 116-118, 120-121

MF Unspecified

CI MAN

SR CA

LC STM Files: CA, CAPLUN, TOXLIB

1 REFERENCES IN FILE CA (1-67 TO DATE)

1 REFERENCES IN FILE CAPLUN (19-7 TO DATE)

REFERENCE 1: 1.1:14-23

LIFE ANSWER 14 OF 16 REGISTRY COPYRIGHT 1993 ACS

EN 152208-02-1 REGISTRY

CH Desaturase, fatty acid *Brassica napus* clone BNS gene fad3 reduced) (CC1) (CA INDEX NAME)

OTHER NAMES:

CH *Brassica napus* fatty acid desaturase *Brassica napus* clone BNS gene fad3)

EC PROTEIN SEQUENCE

SQL 377

SEQ 1 MVAVDQSN ANQDEENPQ AQPPKIGM EAGLPERCKV RSRLESEYV  
 51 ADIFATNAL AVAAVYDSW FFWPIAWAQ GTLPWALFVL CHICGRGFES

101 DIFLNLVNS HIRSPILVP YRWRKISHET RRYNCHVEN LEXWVILPEK

151 IYNNLSHETP ILNTYPLPH LATPLYLWYR SPKECKHYN EYCSLPAPSE

201 RRLIATLTD WSIMLATVY LFLVGPVIV LRYGVPIYII FVMWLDVNTY

251 LHHGHGDLRL PWYRGHEWSY LRGGLTTIDE DYGFNNIEH DIGTHVHHL

=====

KATHLEEN FULLER BT.LIBRARY 308-4290

351 EPQIPHYHLV DATHSAKHVL GRYYREPKTS GAIPHVLVES LVASIKEDHY

351 VDETSDVEFY ETDPDLYVYA SDKSEIN

HITS AT: 91-96, 123-138, 251-256, 295-299

MF Unspecified

CI MAN

SE CA

LC STN Files: CA, CAPLUS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 12:47:48

1.6 ANSWER 15 F 15 REGISTRY COPYRIGHT 1997 ACS

RI 152208-01-0 REGISTRY

CI Desaturase, fatty acid .omega.3- (Brassica napus chloroplast-encoded clone BND gene-fact precursor reduced) (SCI) (CA INDEX NAME)

OTHER NAMES:

CI .omega.3 fatty acid desaturase (Brassica napus chloroplast clone BND gene-fact precursor)

PI PROTEIN SEQUENCE

QCL 329

SEQ 1 MNYVETLAI VPALAGWAY LNNWLAWPLY WIAQGIMFWA LFLVGHDCGH

=====

11 GPEKDHGKRN QVGHGHSSE ILVPYHGMEL SRATHRQNHG HVENDESWHP

=====

111 MNEKIYHLD KTRFFETTL PLTILANPFY LWAESEKKG SHYHFDSDLF

111 LKPEKNVIT STACTAHAV LLVGLNEVNG PMQMLKLYVI PYWINVMWLD

111 ETVYHNGH ESKLWYRGK EWVTLGGIT TLDSDYGLIN NTHHDICTHV

=====

111 IHHLEQCHP YHVEATHAA KPVLGKYYRE PDKSGFLPLH LGLILAKSIK

===

111 EHHFUSIEDD WYVEADGNI YGHIEVTAE

HITS AT: 46-51, 51-60, 116-117, 212-253

MF Unspecified

CI MAN

SE CA

LC STN Files: CA, CAPLUS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 12:47:49

1.6 ANSWER 16 F 16 REGISTRY COPYRIGHT 1997 ACS

RI 149956-03-6 REGISTRY

CI Desaturase, fatty acid .DELTA.12- Arabidopsis thaliana clone pFadx-2 fragment reduced (SCI) (CA INDEX NAME)

OTHER NAMES:

CI .DELTA.12 desaturase fragment Arabidopsis thaliana clone pFadx-2 olefinid

PI PROTEIN SEQUENCE

QCL 156

SEQ 1 LTYVRAFTN WAINVATILT TLQMPSEEDR ERFDFGAPPP FNIADIFAAI

11 PRHCWVENPW MMLFYVEDV AIVFGLAAVA AYFNNWLLWP LYWFAQGTMF

101 WAINVLDHDC GHGSESNQPA LNSVAGHLLH SSILVPYHGW RISHETHEQN

=====

101 HGEVEN

=

HITS AT: 103-112, 144-151

MF Unspecified

CI MAN

SE CA

LC STN Files: CA, CAPLUS, TOXLIT

KATHLEEN FULLER BT/LIBRARY 308-4290



1 REFERENCES IN FILE CA (1967 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 119:153376

126 ANSWER 27 OF 35 REGISTRY COPYRIGHT 1967 ACS

EN 149956-02-5 REGISTRY

EN Desaturase, fatty acid .DELTA.15- (corn clone pPCR20 fragment reduced (9CI) (CA INDEX NAME)

OTHER NAMES:

EN .DELTA.-15 desaturase fragment (Zea mays clone pPCR10)

ES PROTEIN SEQUENCE

SQL 126

SEQ 1 HHQNHSHIR DESWHFITEK LYEQLEPRTE KLEFTTFEL LAEPVYLLYE

=====

51 SPCKLSHPEL PDSDFSPKE KSDVMNSTC WCIMLASLLA MACAFGPLQV  
101 LKMGIEYLV EFWIDNTY LRRHGH

=====

HITS AT: 1-3, 122-126

MF Unspecified

CI MAN

SE CA

IC STN Files: CA, CAPLUS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 119:153376

126 ANSWER 28 OF 35 REGISTRY COPYRIGHT 1967 ACS

EN 149956-01-4 REGISTRY

EN Desaturase, fatty acid .DELTA.15- (soybean clone pSFD-118bwp reduced (9CI) (CA INDEX NAME)

OTHER NAMES:

EN .DELTA.-15 desaturase (Glycine max clone pSFD-118bwp plastid)

EN .omega.-3 fatty acid desaturase (Glycine max chloroplast clone GMD gene fadD)

ES PROTEIN SEQUENCE

SQL 453

SEQ 1 MATWYEQKQG LKSLAPVPEK PRTGAALST GENEFLITNK VVAGPKFQQL

51 RCHLRPNWGF LKMSAPLVA FIEEBQKSNQ LTINGTNGVER EKLPEFDPGA  
101 PPPFNLAHIE AATPHRCUVE DEWRSMSTYV KDVIAVEGLA AAAYINNWL  
151 VWFLYWAAQK TMEWALEYIC HDQGHQSENI NSELNQVVGK LLESSLVPY

=====

201 HGWRKSHETH HQHGHAFND ESWHPLPEK FFLDVTTEM LEETAPPELL

=====

251 AEPVYLFERS EGTGSHFDF SSDLFVPNER KDVITSTACW AAMLGLLVGL

301 GFVAGPIQLL KLYGVFYVIF VMWLDLVTVL HRRGHREKLP WYRGKEWSYL

=====

351 RGHITLIRD YGWNNIHRD LGTHVIHHLF PQIPHYELVE ATEAAKPVEG

=====

401 KYKREPPFSA APLPFELICE LIESFETDHF VSDTGDVVYY QTDSKINGSS

451 KLE

HITS AT: 171-175, 207-214, 301-335, 374-378

MF Unspecified

CI MAN

SE CA

IC STN Files: CA, CAPLUS, TOXLIT

2 REFERENCES IN FILE CA (1967 TO DATE)

2 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 120:47048

REFERENCE 2: 119:153-76

126 ANSWER 29 OF 36 REGISTRY COPYRIGHT 1987 ACS

EN 149956-00-3 REGISTRY

CU Desaturase, fatty acid DELTA.15- soybean clone pXF1 reduced) (9CI)  
(CA INDEX NAME)

OTHER NAMES:

CU DELTA.15 desaturase (Glycine max clone pXF1 microsomal)

CU Omega-3 fatty acid desaturase (Glycine max clone GM3 gene fad3)

EC PROTEIN SEQUENCE

SQL 380

SEQ 1 MNTETETAY AANNQYQNG SSEDEDFCAP PPFKIAEIPA SIPKHCVKKN  
11 FWRSLSTLE DVNIAALVA AAHFDHWWL WLYCFIQGT MFWALFVLGH

101 DCHGSEFDS PLNSIVGHI LESSIAPYE GWEISHFTHH QHGHIEKDE

101 SWNFTETNY KNDSDMTALI FETVPPPLEV YPIYLFSESP GREGSHFNPY

101 SILSTPPEEK GIALSTLWA TMSLLIYLS FITSPLLVLK LYGIPYWIFV

101 MWLFVTTLE HSHRQHLPW YGKRWYIR GGLTTVIRY GRIYNIHEDI

101 GCHVINHLEP QTERYHNEA TQAAPNLD YREPEFSAP LPTHLIKYLI

101 QMPPQDPYS FIDNYYQT ISLLIESQED

HITS AT: 130-134, 136-143, 160-165, 303-307

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

REFERENCES IN FILE CA (1987 TO DATE)

REFERENCES IN FILE CAPLUS (1987 TO DATE)

REFERENCE 1: 120:470-81

REFERENCE 1: 119:153-76

126 ANSWER 30 OF 36 REGISTRY COPYRIGHT 1987 ACS

EN 149955-99-7 REGISTRY

CU Desaturase, fatty acid DELTA.15- Brassica napus clone pNSFd-2  
C-terminal fragment reduced: (9CI) (CA INDEX NAME)

OTHER NAMES:

CU DELTA.15 glycerolipid desaturase Brassica napus clone pNSFd-2  
partial

EC PROTEIN SEQUENCE

SQL 404

SEQ 1 PPFQASHSP EFENSHAWA INVTTHTTD SEUSEPIEEE PHTQRFDPGA

11 PPFENALIR AAIPHCWVK NWKSMYVW RELATVFAIA AGAAYLINWL

101 MWPLYWLAGS THFWALFVLG HCGHSEFEN DEALNCVCH LESSIAPYE

101 GWEISHFTH HGNHSEVEND ESWHETKEHI YELDEFTAF EKFTEPLVML

101 AYPEYMAES PGKKGSHYHE FDDLFLPKEK NDULTSTACW TAMAVLINVL

101 DFTNGSHQML KLYVTPWIN MWLDEFVTL HARGHEDELP WYKREWSYL

101 KGLITELSD YGLNNIHHD LGTHVINHLE PDPHYHAE ATEAAKPVLG

101 HYREPPDESS PLPLHLMHIL AKSIKEDHYV SDEGDIVVYE ADPNLYGEIK

101 VTAE

HITS AT: 121-125, 157-164, 181-185, 324-328

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

KATHLEEN FULLER BT/LIBRARY 308-4200

1 REFERENCES IN FILE CA (1967 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 119:153246

126 ANSWER 31 OF 36 REGISTRY COPYRIGHT 1987 ACS

EN 149955-98-6 REGISTRY

CU Desaturase, fatty acid .DELTA.-11- (Brassica napus clone pPNSF3-f2  
C-terminal fragment reduced) (91) (CA INDEX NAME)

OTHER NAMES:

CU .DELTA.-11 glycerolipid desaturase (Brassica napus clone pPNSF3-2  
microsomal)

EN PROTEIN SEQUENCE

SQL 378

SEQ 1 LTVIASSSPPP IEEEPKQRF DEGAIPPPHL ADIRAAIPKH CWVENPWKSH  
51 SYVPELAIN YALAGAYL NWLVWPLYW IAGTHFWAL FVLGHDCGEG

101 .SEVLPENIC NVHLLKSI LVPYQWRIS HETHQNHCH VENDESWEHM

151 .PEIYKSLDK PTEFFRTLP LVLAYPPYL WASSPGKGS HYHDSSEFL

161 PFEENDLTS CANTANAL LVLNFWVSP HQLFLYVIP YWINVMWLD

181 VYIHHHHE DKUWYDRE WYLLGGLTT LFDYGLINN EHHDGTHV

201 HHFFQIRSY HNEATEAAK FVLKYYREP DKGGLLEHL LGILAKSK

231 DHEVDEGCV VVEADENIN GHVNTAE

HITS AT: 9-43, 111-114, 151-153, 193-242

MF Unspecified

CI MAN

SA CA

10 STN Files: CA, CAPLUS, TOXNET

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 119:153246

126 ANSWER 31 OF 36 REGISTRY COPYRIGHT 1987 ACS

EN 149955-97-5 REGISTRY

CU Desaturase, fatty acid .DELTA.-11- (Arabidopsis thaliana clone  
pACF2-1 reduced) (91) (CA INDEX NAME)

OTHER NAMES:

CU .DELTA.-11 fatty acid desaturase (Arabidopsis thaliana clone pACF2-2  
plastid)

CU .omega.-3 fatty acid desaturase Arabidopsis thaliana chloroplast  
clone CPl gene (adl precursor)

CU .omega.-3-Fatty acid desaturase Arabidopsis thaliana clone g45)

EN PROTEIN SEQUENCE

SQL 446

SEQ 1 HANENLSEDE LPLPPIYTT HKNFLSMN HEPKSLSSS YKSSSPLSF  
51 GLNEDGSTR NWALNTHPL IYIFEECHL EELNQRDOP GAFFPENLAD

101 IRALPHEW VEPWESLKY VAEVAIVFA LAAGAYLNN WLVWPLYWLA

151 QGTHWALFY LKDDGKCF SDIKLNIV GHLESLILV PYQWRISK

201 THQKRGHYE NGENWHMSE HNTLDKPT KFFRTSLPLV ILAYPPYLWA

251 KSGKFGSHY HGGDLFLPK EKKVLTSTA CWTAMALLV CLNETIGPIQ

301 HLKLYGIPYW IEMWLDFTV VHHHSHEOK LKYYKEWS YLAGGLTTLQ

351 RDYGLINNIH HDGTHVIH LPPPIPHYEL VEATEAAKPV LGKYYREPDK

401 SGLPLHLLI ILAKSHEDH YUSDEGEVY YEDPNLYGE VKVREAD

HITS AT: 165-167, 199-206, 323-327, 366-370

KATHLEEN FULLER BT/LIBRARY 308-4290

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

4 REFERENCES IN FILE CA (1967 TO DATE)

4 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 191:297399

REFERENCE 2: 190:184029

REFERENCE 3: 190:47098

REFERENCE 4: 199:133376

1.6 ANSWER 33 OF 36 REGISTRY COPYRIGHT 1997 ACS

EN 149955-96-4 REGISTERED

CN Desaturase, fatty acid DELTA.15- (Arabidopsis thaliana clone pCF3 reduced) (OCL) (CA INDEX NAME)

OTHER NAMES:

CN DELTA.15-desaturase (Arabidopsis thaliana clone pCF3)

CN Omega-3 fatty acid desaturase (Arabidopsis thaliana clone CF3 gene fa13)

FS PROTEIN SEQUENCE

SQL 386

```
SEQ      1  MIVAMDDQETH VNELEGACIE EKEERFDRIA QPPEKIGDIR AAIPKHQWVK
      51  SPSRDMYYTV EDLIAVAALA TAAVYVDSWF LWFLYWAAQG TLFWAIFVLG
     101  HQGGRGEPED IPIDMSVVGH ILSFILVPY HGRERISERTH HONHGHVEND
          =====
     151  ESWVPLEEEN YPELERSTEM MEYTVLEPHL AYELYLCYES PEKEGSHENP
     201  YSELPAEER ELIATSTTOW LIMEVLIAL SEYEGELAVL KVGVPYILF
     251  VWELIATYD HSGCHIEKLF WYRGKWSYL RGLATIDED YGIFNNIHHD
          == ==
     301  IGTHIRHLF POLRHYHND ATKAAHHVLG RYVEEPKTES AIPHLVESL
          =====
     351  VASIRKDEHY SDTCQIVFYE TDPDLVYYAS DESKIN
```

HITS AT: 191-205, 197-199, 191-195, 194-308

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

4 REFERENCES IN FILE CA (1967 TO DATE)

4 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 191:47098

REFERENCE 2: 199:133376

1.6 ANSWER 34 OF 36 REGISTRY COPYRIGHT 1997 ACS

EN 148814-49-7 REGISTERED

CN Desaturase, fatty acid DELTA.15- (Brassica napus clone pBNDES3 gene fa13 reduced) (OCL) (CA INDEX NAME)

OTHER NAMES:

CN Omega.3 Lin. late desaturase (Arabidopsis reduced)

FS PROTEIN SEQUENCE

SQL 383

```
SEQ      1  MIVAMDDQETH VNEEGSARKE EGEDPSAQFP EKIGDIEAAI PEHCWVKSPL
      51  RSMSTVTEDI FAVAAAMIAA VYFDSWFLWP LYVVAQSTLF WAIFVLGHDC
          =====
     101  GHGSEGDIEP LNSUVGHILH SFILVPYH W RLSHRTTHQN HGHVENDESW
          == =====
     151  VELPEKLYEN LPHSTEMLEY TVPLEMLAYP IYLWYRSPGE EGSHFNPYSS
          KATHLEEN FULLER BT/LIBRARY 308-4290
```

201 LEAPSEPKLI ATSTTCWSIM LATLVYLSFL VDFVTVLKVY GVPYIIFVMW  
201 LDVAVYLLHHH GHLEKLPWYF GKWSYLRGG LSTIEFYGI FNNIHHDIGT  
=====  
201 HVVHLEFPQI PHVHLVLAIF AAKHVLGFNY EEPKTSQAP IHLVESLVS  
=====

201 IKHTEYVSET GDIVFYETEE DLYVYASDFS KIN

HITS AT: 98-100, 124-141, 158-262, 301-305

MF Unspecified

CI MAN

CR CA

LC STN Files: CA, CABLUS, TOKKIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CABLUS (1967 TO DATE)

REFERENCE 1: 121:197309

REFERENCE 2: 119:11620

126 ANSWER 34 OF 36 REGISTRY COPYRIGHT 1997 ACS

RI 148734-39-8 REGISTRY

CI Desaturase, linoleate (Syneschoecystis strain PCC 6803 clone csy75-3.5 reduced) (CA INDEX NAME)

OTHER NAMES:

CI DELTA-6-Desaturase (Syneschoecystis clone pSy75-3.5)

CI Desaturase, linoleate (Syneschoecystis strain PCC 6803)

CI GenBank 106-014-derived protein (116-3589)

CI Protein (Syneschoecystis strain PCC 6803 clone csy75-3.5) (116-3589) open reading frame s110262 reduced

FI PROTEIN SEQUENCE

ML 359

SEQ 1 MLTAARKIPT DDEGFAVIN QEDVAYFAEH GLTQSDNPSM YLKTLLIIVLW  
21 LDFAMAFVLF AFVIFVRL QCIDLAIALA AFSENVGHDA NNNAYSSNPH  
=====

21 LNNVLSNTYD EYHLSFLWR YHHVYHHTY TNLGHDVEI HGDGAVEMSP  
=====

21 EQFHUSIYRF QQFYIWMYD FIPFYWFLD VYLVLNKGY HDHKIPPFQD

21 LRIAGLLGIH LNLGYWFL PLALGFSIPE VLGASVTYM TYGIVVCTIF

21 LIAHVLNTE EALPDGELGA LBDMAICDI RTTANPATNN PFWNWFCGSL

21 NGLVTHLEFP NT THIRNPQL ENICKDVCJE FSVYKQVYPT FKAALASNYR  
=====

21 WREAGISPS

HITS AT: 88-91, 128-141, 303-306

MF Unspecified

CI MAN

CR CA

LC STN Files: CA, CABLUS, TOKKIT, USPATEFULL

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CABLUS (1967 TO DATE)

REFERENCE 1: 126:19906

REFERENCE 2: 126:70918

REFERENCE 3: 119:154315

REFERENCE 4: 119:64918

126 ANSWER 35 OF 36 REGISTRY COPYRIGHT 1997 ACS

RI 131198-85-1 REGISTRY

CI Desaturase, acyl coenzyme A (Saccharomyces cerevisiae reduced) (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE

KATHLEEN FULLER BT/LIBRARY 308-4290

• SQL 510

```

SEQ      1 MPTSGTTIEL IDQFPKDD S ASSGIVDEVD LTEANILATG LNKKAPRIVN
      51 GFGSILMGSK MVSVEFDKFG NERKSNLDEL LEFDNQEKKE AKTKIHISEQ
     101 PWTLLNNWHQH LNWLNMMVAV GMPMIGWYFA LSGKVPLHLN VFLPSVEYYA
     151 VGGVSITAGY HRLWSHRSYS AHWPLRLFYA LFGCASVEGS AKWWGHSHEI
                                     ===
     201 HHRNTDTLAD PYDAREGLWY SHMGWMLLEP NPFYKAFADI TDMTDLWTIE
                                     ===
     251 FQHHYILLM LLTASVITPL ICGYFENDYM GGLIYAGFIR VFVLCQATEC
     301 INSMARYIST QPFDORRTEF DNWITAIVTF GEGYNERHEE FPTDYRNAIK
                                     =====
     351 WYQYDPTKVI IYLTSLVGLA YDLKKFSQIA LEEALIQEQ KHINKKKAKI
     401 NWSIVLTDLP MWDEQTFIAM SKENKGLVII SGIVHDVSGY ISEHFGGETL
     451 IKPALGPDAT KAFSGGVYRH SNAAQNVLAB MRCVAVIFESK NSAIEMASKK
     501 GEIYETGFFF

```

HITS AT: 195-202, 335-339

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 114:18574